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OM protein - protein search, using sw model

Run on: May 15, 2006, 16:16:32 ; Search time 47 Seconds
(without alignments)
28.145 Million cell updates/sec

Title: US-09-865-281A-1
Perfect score: 91
Sequence: 1 KNREDPGKQLYNVEA 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	100.0	16	2 US-09-070-907-1	Sequence 1, Appli
2	91	100.0	16	2 US-09-623-548A-1536	Sequence 1536, Ap
3	91	100.0	16	2 US-09-657-276-1536	Sequence 1536, Ap
4	91	100.0	63	1 US-08-447-411-24	Sequence 24, Appl
5	91	100.0	63	1 US-08-447-411-63	Sequence 63, Appl
6	91	100.0	63	1 US-08-662-227-20	Sequence 20, Appl
7	91	100.0	63	2 US-09-017-947-20	Sequence 20, Appl
8	91	100.0	63	2 US-09-925-442-20	Sequence 20, Appl
9	91	100.0	310	2 US-09-834-309-7	Sequence 7, Appli
10	91	100.0	310	2 US-09-834-309-8	Sequence 8, Appli
11	91	100.0	310	2 US-09-834-309-9	Sequence 9, Appli
12	91	100.0	1663	1 US-08-793-126-1	Sequence 1, Appli
13	91	100.0	1663	2 US-09-132-271-1	Sequence 1, Appli
14	91	100.0	1663	2 US-09-142-334-22	Sequence 22, Appl
15	80	87.9	63	1 US-08-447-411-26	Sequence 26, Appl
16	79	86.8	63	1 US-08-447-411-27	Sequence 27, Appl
17	73	80.2	63	1 US-08-447-411-25	Sequence 25, Appl
18	73	80.2	308	2 US-09-582-761B-26	Sequence 26, Appl
19	73	80.2	330	2 US-09-582-761B-37	Sequence 37, Appl
20	73	80.2	929	2 US-09-582-761B-27	Sequence 27, Appl
21	60	65.9	11	2 US-09-039-060A-6	Sequence 6, Appli
22	60	65.9	11	2 US-08-495-606E-37	Sequence 37, Appl
23	60	65.9	11	4 PCT-US94-01234-37	Sequence 37, Appl
24	60	65.9	11	4 PCT-US94-01263-7	Sequence 7, Appli
25	52	57.1	1333	1 US-08-447-411-76	Sequence 76, Appl
26	52	57.1	1333	1 US-08-662-227-34	Sequence 34, Appl
27	52	57.1	1333	2 US-09-017-947-34	Sequence 34, Appl

28	57.1	1333	2	US-09-925-442-34	Sequence 34, Appl
29	56.0	10	1	US-08-634-060-33	Sequence 33, Appl
30	56.0	10	1	US-08-700-846-5	Sequence 5, Appli
31	46	50.5	1493	2 US-09-713-273A-20	Sequence 20, Appl
32	44	48.4	193	2 US-09-248-796A-20794	Sequence 20794, A
33	44	48.4	2628	2 US-09-413-814-11	Sequence 11, Appl
34	43	47.3	28	1 US-08-448-603A-7	Sequence 7, Appli
35	43	47.3	28	2 US-09-134-075-7	Sequence 7, Appli
36	43	47.3	28	2 US-09-492-739-7	Sequence 7, Appli
37	43	47.3	28	2 US-09-966-931A-7	Sequence 7, Appli
38	43	47.3	63	1 US-08-447-411-23	Sequence 23, Appl
39	43	47.3	63	1 US-08-447-411-62	Sequence 62, Appl
40	43	47.3	63	1 US-08-662-227-19	Sequence 19, Appl
41	43	47.3	63	2 US-09-017-947-19	Sequence 19, Appl
42	43	47.3	63	2 US-09-925-442-19	Sequence 19, Appl
43	43	47.3	95	2 US-09-270-767-39763	Sequence 39763, A
44	43	47.3	95	2 US-09-270-767-54980	Sequence 54980, A
45	43	47.3	467	2 US-10-040-802-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-070-907-1
; Sequence 1, Application US/09070907
; Patent No. 6238667
; GENERAL INFORMATION:
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: METHOD OF AFFINITY CROSS-LINKING BIOLOGICALLY ACTIVE
; FILE REFERENCE: 35629
; CURRENT APPLICATION NUMBER: US/09/070,907
; CURRENT FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.0 - beta
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AMINO ACID
; OTHER INFORMATION: SEQUENCE DERIVED FROM Cd3 peptide
US-09-070-907-1

Query Match 100.0%; Score 91; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.4e-09; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0;
QY 1 KNREDPGKQLYNVEA 16
|||||
Db 1 KNREDPGKQLYNVEA 16
|||||
RESULT 2
US-09-623-548A-1536
; Sequence 1536, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17

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; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1536
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-1536

Query Match          100.0%; Score 91; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.4e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWDPGKQLYNVEA 16
   |||||
Db 1 KNRWDPGKQLYNVEA 16

RESULT 3
US-09-657-276-1536
; Sequence 1536, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1536
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-1536

Query Match          100.0%; Score 91; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.4e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWDPGKQLYNVEA 16
   |||||
Db 1 KNRWDPGKQLYNVEA 16

RESULT 4
US-08-447-411-24
; Sequence 24, Application US/08447411
; Patent No. 5773243
; GENERAL INFORMATION:
; APPLICANT: FRITZINGER, DAVID C.
```

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; APPLICANT: BREDEHORST, REINHARD
; APPLICANT: VOGEL, CARL-WILHELM
; TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,411
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/043,747
; FILING DATE: 07-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5773243man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-101-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-447-411-24

Query Match          100.0%; Score 91; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWDPGKQLYNVEA 16
   |||||
Db 9 KNRWDPGKQLYNVEA 24

RESULT 5
US-08-447-411-63
; Sequence 63, Application US/08447411
; Patent No. 5773243
; GENERAL INFORMATION:
; APPLICANT: FRITZINGER, DAVID C.
; APPLICANT: BREDEHORST, REINHARD
; APPLICANT: VOGEL, CARL-WILHELM
; TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,411
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/043,747
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5773243man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-101-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248955 OPAT UR
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-447-411-63

Query Match 100.0%; Score 91; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKQLYNVEA 16
|||||

DB 9 KNRWEDPGKQLYNVEA 24

RESULT 6
US-08-662-227-20
Sequence 20, Application US/08662227
Patent No. 5923320
GENERAL INFORMATION:
APPLICANT: VOGEL, CARL-WILHELM
APPLICANT: BREDEHORST, REINHORST
APPLICANT: KOCK, MICHAEL
APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCVF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,227
FILING DATE: 14-JUN-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-0107-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-662-227-20

Query Match 100.0%; Score 91; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKQLYNVEA 16
|||||

DB 9 KNRWEDPGKQLYNVEA 24

RESULT 7
US-09-017-947-20
Sequence 20, Application US/09017947
Patent No. 6303754
GENERAL INFORMATION:
APPLICANT: VOGEL, CARL-WILHELM
APPLICANT: BREDEHORST, REINHORST
APPLICANT: KOCK, MICHAEL
APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCVF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,947
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/662,227
FILING DATE: 14-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-0107-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-017-947-20

Query Match 100.0%; Score 91; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKQLYNVEA 16
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DB 9 KNRWEDPGKQLYNVEA 24

RESULT 8
US-09-925-442-20

; Sequence 20, Application US/09925442
; Patent No. 6607897
; GENERAL INFORMATION:
; APPLICANT: VOGEL, CARL-WILHELM
; BREDEHORST, REINHORST
; KOCK, MICHAEL
; FRITZINGER, DAVID
; TITLE OF INVENTION: RECOMBINANT PROCVF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/925,442
; FILING DATE: 10-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/017,947
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-0107-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-925-442-20

Query Match 100.0%; Score 91; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWDPGKQLYNVEA 16
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Db 9 KNRWDPGKQLYNVEA 24

RESULT 9
US-09-834-309-7
; Sequence 7, Application US/09834309
; Patent No. 6820011
; GENERAL INFORMATION:
; APPLICANT: Chen, Xiaojiang
; APPLICANT: Holers, V. Michael
; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND USE
; FILE REFERENCE: 2848-43
; CURRENT APPLICATION NUMBER: US/09/834,309
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-834-309-7

Query Match 100.0%; Score 91; DB 2; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWDPGKQLYNVEA 16
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Db 224 KNRWDPGKQLYNVEA 239

RESULT 10

US-09-834-309-8
; Sequence 8, Application US/09834309
; Patent No. 6820011
; GENERAL INFORMATION:
; APPLICANT: Chen, Xiaojiang
; APPLICANT: Holers, V. Michael
; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND USE
; FILE REFERENCE: 2848-43
; CURRENT APPLICATION NUMBER: US/09/834,309
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-309-8

Query Match 100.0%; Score 91; DB 2; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWDPGKQLYNVEA 16
| | | | | | | | | | | | | | | |
Db 224 KNRWDPGKQLYNVEA 239

RESULT 11

US-09-834-309-9
; Sequence 9, Application US/09834309
; Patent No. 6820011
; GENERAL INFORMATION:
; APPLICANT: Chen, Xiaojiang
; APPLICANT: Holers, V. Michael
; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND USE
; FILE REFERENCE: 2848-43
; CURRENT APPLICATION NUMBER: US/09/834,309
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-309-9

Query Match 100.0%; Score 91; DB 2; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWDPGKQLYNVEA 16
| | | | | | | | | | | | | | | |
Db 224 KNRWDPGKQLYNVEA 239

RESULT 12

US-08-793-126-1
; Sequence 1, Application US/08793126
; Patent No. 5849297

GENERAL INFORMATION:
APPLICANT: Harrison, Richard Alexander
TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,126
FILING DATE: 07-FEB-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 102286.377
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1663 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-793-126-1

Query Match 100.0%; Score 91; DB 1; Length 1663;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNWEDPGKOLYNVEA 16
Db 1217 KNWEDPGKOLYNVEA 1232

RESULT 13
US-09-132-271-1
Sequence 1, Application US/09132271
Patent No. 6221657
GENERAL INFORMATION:
APPLICANT: Harrison, Richard Alexander
TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/132,271
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/793,126

FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 102286.377
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1663 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-132-271-1

Query Match 100.0%; Score 91; DB 2; Length 1663;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNWEDPGKOLYNVEA 16
Db 1217 KNWEDPGKOLYNVEA 1232

RESULT 14
US-09-142-334-22
Sequence 22, Application US/09142334
Patent No. 6268485
GENERAL INFORMATION:
APPLICANT: Farries, Timothy C.
TITLE OF INVENTION: Down-Regulation Resistant C3 Convertase
FILE REFERENCE: 4-30443/A/IMU/PCT
CURRENT APPLICATION NUMBER: US/09/142,334
EARLIER FILING DATE: 1999-04-15
PCT/GB97/00603
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 1663
TYPE: PRT
ORGANISM: Homo sapiens
US-09-142-334-22

Query Match 100.0%; Score 91; DB 2; Length 1663;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNWEDPGKOLYNVEA 16
Db 1217 KNWEDPGKOLYNVEA 1232

RESULT 15
US-08-447-411-26
Sequence 26, Application US/08447411
Patent No. 5773243
GENERAL INFORMATION:
APPLICANT: FRITZINGER, DAVID C.
APPLICANT: BREDEHORST, REINHARD
APPLICANT: VOGEL, CARL-WILHELM
TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.

```

;
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,411
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/043,747
; FILING DATE: 07-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5773243man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-101-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-447-411-26

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Query Match      87.9%  Score 80;  DB 1;  Length 63;
Best Local Similarity 81.2%  Pred. No. 2.7e-06;
Matches 13;  Conservative 3;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1  KNRWEDPGKQLYNVEA 16
       :||||:|||||
Db      9  RNRWEEPGQLYNVEA 24

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Search completed: May 15, 2006, 16:17:50
Job time : 48 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 16:27:41 ; Search time 164 Seconds
(without alignments)
40.764 Million cell updates/sec

Title: US-09-865-281A-1

Perfect score: 91

Sequence: 1 KNWEDPGKQLYNVEA 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	100.0	16	3	US-09-865-281A-1
2	91	100.0	16	5	US-10-795-081A-1
3	91	100.0	16	6	US-11-066-697-1536
4	91	100.0	63	3	US-09-925-442-20
5	91	100.0	94	4	US-10-424-599-219407
6	91	100.0	310	3	US-09-834-309-7
7	91	100.0	310	3	US-09-834-309-8
8	91	100.0	310	3	US-09-834-309-9
9	91	100.0	705	4	US-10-379-747-4
10	91	100.0	935	5	US-10-887-775-32
11	91	100.0	1255	5	US-10-497-073-17
12	91	100.0	1288	5	US-10-741-600-1326
13	91	100.0	1540	5	US-10-450-763-56335
14	91	100.0	1638	5	US-10-884-813-8
15	91	100.0	1638	5	US-10-884-813-12
16	91	100.0	1663	3	US-09-875-519A-22
17	91	100.0	1663	3	US-09-842-758-41
18	91	100.0	1663	4	US-10-379-747-2
19	91	100.0	1663	4	US-10-174-333-41
20	91	100.0	1663	5	US-10-741-600-1327
21	91	100.0	1663	5	US-10-928-312-2
22	91	100.0	1663	5	US-10-884-813-2
23	91	100.0	1663	5	US-10-884-813-6
24	91	100.0	1663	5	US-10-884-813-10
25	91	100.0	1663	5	US-10-887-775-30
26	83	91.2	296	4	US-10-398-916-29
27	83	91.2	296	4	US-10-398-916-30

28	83	91.2	300	4	US-10-398-916-13	Sequence 13, Appl
29	82	90.1	105	3	US-09-925-301-1490	Sequence 1490, Ap
30	80	87.9	1663	5	US-10-989-891-141	Sequence 141, Appl
31	76	83.5	300	4	US-10-398-916-11	Sequence 11, Appl
32	76	83.5	300	4	US-10-398-916-15	Sequence 15, Appl
33	73	80.2	300	4	US-10-398-916-9	Sequence 9, Appl
34	73	80.2	312	4	US-10-398-916-17	Sequence 17, Appl
35	73	80.2	409	4	US-10-466-655-6	Sequence 6, Appl
36	73	80.2	1663	3	US-09-842-758-43	Sequence 43, Appl
37	73	80.2	1663	4	US-10-174-333-43	Sequence 43, Appl
38	71	78.0	1661	3	US-09-842-758-42	Sequence 42, Appl
39	71	78.0	1661	4	US-10-174-333-42	Sequence 42, Appl
40	69	75.8	296	5	US-10-505-546-10	Sequence 10, Appl
41	60	65.9	11	4	US-10-408-849-6	Sequence 6, Appl
42	52	57.1	1333	3	US-09-925-442-34	Sequence 34, Appl
43	46.5	51.1	500	4	US-10-282-122A-57243	Sequence 57243, A
44	46	50.5	329	4	US-10-425-115-197051	Sequence 197051, A
45	46	50.5	437	4	US-10-424-599-190068	Sequence 190068, A

ALIGNMENTS

RESULT 1

US-09-865-281A-1

; Sequence 1, Application US/09865281A

; Publication No. US20030103984A1

; GENERAL INFORMATION:

; APPLICANT: Kohler, Heinz

; TITLE OF INVENTION: FUSION PROTEINS OF BIOLOGICALLY ACTIVE PEPTIDES AND ANTIBODIES

; FILE REFERENCE: 411.35629PC2

; CURRENT APPLICATION NUMBER: US/09/865,281A

; CURRENT FILING DATE: 2001-05-29

; PRIOR APPLICATION NUMBER: 09/070,907

; PRIOR FILING DATE: 1998-05-04

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (1)..(16)

; OTHER INFORMATION: Synthesized peptide with sequence derived from position 1217-123.

US-09-865-281A-1

Query Match 100.0%; Score 91; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNWEDPGKQLYNVEA 16

Db 1 KNWEDPGKQLYNVEA 16

RESULT 2

US-10-795-081A-1

; Sequence 1, Application US/10795081A

; Publication No. US2005003303A1

; GENERAL INFORMATION:

; APPLICANT: Kohler, Heinz

; TITLE OF INVENTION: TRANS-MEMBRANE-ANTIBODY INDUCED INHIBITION OF APOPTOSIS

; FILE REFERENCE: 411.35629AP3

; CURRENT APPLICATION NUMBER: US/10/795,081A

; CURRENT FILING DATE: 2004-03-05

; PRIOR APPLICATION NUMBER: 60/451,980

; PRIOR FILING DATE: 2003-03-05

; PRIOR APPLICATION NUMBER: 09/865,281

; PRIOR FILING DATE: 2001-05-29

; PRIOR APPLICATION NUMBER: 09/070,907

; PRIOR FILING DATE: 1998-05-04

; NUMBER OF SEQ ID NOS: 14

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(16)
; OTHER INFORMATION: Synthesized peptide with sequence derived from position 1217-1232
US-10-795-081A-1

Query Match          100.0%; Score 91; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNRWDPGKQLYNVEA 16
       |||||
Db      1 KNRWDPGKQLYNVEA 16

RESULT 3
US-11-066-697-1536
; Sequence 1536, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibadeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1536
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-1536

Query Match          100.0%; Score 91; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNRWDPGKQLYNVEA 16
       |||||
Db      1 KNRWDPGKQLYNVEA 16

RESULT 4
US-09-925-442-20
; Sequence 20, Application US/09925442
; Patent No. US2002010346A1
; GENERAL INFORMATION:
; APPLICANT: VOGEL, CARL-WILHELM
; BREDEHORST, REINHORST
; KOCK, MICHAEL
; FRITZINGER, DAVID
; TITLE OF INVENTION: RECOMBINANT PROCVF
; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/925,442
; FILING DATE: 10-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/017,947
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-0107-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-925-442-20

Query Match          100.0%; Score 91; DB 3; Length 63;
Best Local Similarity 100.0%; Pred. No. 7.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNRWDPGKQLYNVEA 16
       |||||
Db      9 KNRWDPGKQLYNVEA 24

RESULT 5
US-10-424-599-219407
; Sequence 219407, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 219407
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(94)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_40150C.1.pap
US-10-424-599-219407
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Query Match 100.0%; Score 91; DB 4; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.1e-06; Indels 0;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1 KNRWDPGKQLYNVEA 16
|||||
Db 43 KNRWDPGKQLYNVEA 58

RESULT 6

US-09-834-309-7
; Sequence 7, Application US/09834309
; Publication No. US2004000538A1

GENERAL INFORMATION:

; APPLICANT: Chen, Xiaojiang
; APPLICANT: Holers, V. Michael
; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND USE
; FILE REFERENCE: 2848-43
; CURRENT APPLICATION NUMBER: US/09/834,309
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-834-309-7

Query Match 100.0%; Score 91; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 3.7e-06; Indels 0;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1 KNRWDPGKQLYNVEA 16
|||||
Db 224 KNRWDPGKQLYNVEA 239

RESULT 7

US-09-834-309-8
; Sequence 8, Application US/09834309
; Publication No. US2004000538A1

GENERAL INFORMATION:

; APPLICANT: Chen, Xiaojiang
; APPLICANT: Holers, V. Michael
; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND USE
; FILE REFERENCE: 2848-43
; CURRENT APPLICATION NUMBER: US/09/834,309
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-834-309-8

Query Match 100.0%; Score 91; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 3.7e-06; Indels 0;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1 KNRWDPGKQLYNVEA 16
|||||
Db 224 KNRWDPGKQLYNVEA 239

RESULT 8

US-09-834-309-9
; Sequence 9, Application US/09834309
; Publication No. US2004000538A1

GENERAL INFORMATION:

; APPLICANT: Holers, V. Michael
; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND USE
; FILE REFERENCE: 2848-43
; CURRENT APPLICATION NUMBER: US/09/834,309
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-834-309-9

Query Match 100.0%; Score 91; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 3.7e-06; Indels 0;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1 KNRWDPGKQLYNVEA 16
|||||
Db 224 KNRWDPGKQLYNVEA 239

RESULT 9

US-10-379-747-4
; Sequence 4, Application US/10379747
; Publication No. US20040023874A1

GENERAL INFORMATION:

; APPLICANT: Burgess, Catherine E.;
; APPLICANT: Chant, John S.;
; APPLICANT: Chaudhuri, Amitabha;
; APPLICANT: Edinger, Shlomit R.;
; APPLICANT: Gangolli, Esha A.;
; APPLICANT: Malyankar, Uriel M.;
; APPLICANT: Miller, Charles E.;
; APPLICANT: Ooi, Chean Eng;
; APPLICANT: Ort, Tatiana A.;
; APPLICANT: Patturajan, Meera;
; APPLICANT: Rastelli, Luca;
; APPLICANT: Rieger, Daniel K.;
; APPLICANT: Shinkets, Richard A.;
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-568B
; CURRENT APPLICATION NUMBER: US/10/379,747
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 60/365,034
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/366,420
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 60/365,477
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-379-747-4

Query Match 100.0%; Score 91; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 8.7e-06; Indels 0;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1 KNRWDPGKQLYNVEA 16
|||||
Db 259 KNRWDPGKQLYNVEA 274

RESULT 10

US-10-887-775-32
; Sequence 32, Application US/10887775
; Publication No. US20050130182A1

```
; GENERAL INFORMATION:
; APPLICANT: MESSER, Jeffrey
; APPLICANT: BENJAMIN, Dennis
; APPLICANT: VATH, James
; APPLICANT: SIGEL, Eric
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: ENOMETRIOSIS
; FILE REFERENCE: PPI-149
; CURRENT APPLICATION NUMBER: US/10/887,775
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/486,379
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: 60/533,430
; PRIOR FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: 60/575,269
; PRIOR FILING DATE: 2004-05-08
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 935
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-887-775-32

Query Match      100.0%; Score 91; DB 5; Length 935;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNRWDPGKQLYNVEA 16
      |||||||
Db      489 KNRWDPGKQLYNVEA 504

RESULT 11
US-10-497-073-17
; Sequence 17, Application US/10497073
; Publication No. US20050048584A1
; GENERAL INFORMATION:
; APPLICANT: Biovision AG
; TITLE OF INVENTION: Method for detecting Alzheimer's disease and differentiating
; TITLE OF INVENTION: Alzheimer's disease from other demential diseases, associated
; TITLE OF INVENTION: peptides and the use thereof
; FILE REFERENCE: C3f-PCT
; CURRENT APPLICATION NUMBER: US/10/497,073
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: DE10158180
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: PCT/DE02/04360
; PRIOR FILING DATE: 2002-11-27
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-497-073-17

Query Match      100.0%; Score 91; DB 5; Length 1255;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNRWDPGKQLYNVEA 16
      |||||||
Db      809 KNRWDPGKQLYNVEA 824

RESULT 12
US-10-741-600-1326
; Sequence 1326, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
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; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1326
; LENGTH: 1288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1326

Query Match      100.0%; Score 91; DB 5; Length 1288;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNRWDPGKQLYNVEA 16
      |||||||
Db      1217 KNRWDPGKQLYNVEA 1232

RESULT 13
US-10-450-763-56335
; Sequence 56335, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: HySeq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56335
; LENGTH: 1540
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (689)..(699)
; OTHER INFORMATION: ANAPHYLATOXIN DOMAIN SIGNATURE domain identified by eMATRIX,
; OTHER INFORMATION: accession number PR000004A, p-value=5.500e-13, raw score of 9.52
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (756)..(1370)
; OTHER INFORMATION: Alpha-2-macroglobulin family domain identified by PFam,
; OTHER INFORMATION: accession name A2M, E-value=0, Pfam score of 1156.5
US-10-450-763-56335

Query Match      100.0%; Score 91; DB 5; Length 1540;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNRWDPGKQLYNVEA 16
      |||||||
Db      1217 KNRWDPGKQLYNVEA 1232

RESULT 14
US-10-884-813-8
; Sequence 8, Application US/10884813
; Publication No. US20050079585A1
; GENERAL INFORMATION:
; APPLICANT: Kolln, Johanna
; APPLICANT: Bredehorst, Reinhard
; APPLICANT: Spillner, Edzard
```

;
; TITLE OF INVENTION: Complement Depletion with Recombinant Human C3 Derivatives
; FILE REFERENCE: P 63782
; CURRENT APPLICATION NUMBER: US/10/884,813
; CURRENT FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1638
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid protein
US-10-884-813-8

Query Match 100.0%; Score 91; DB 5; Length 1638;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWDPGKQLYNVEA 16
|||
Db 1217 KNRWDPGKQLYNVEA 1232

RESULT 15
US-10-884-813-12
; Sequence 12, Application US/10884813
; Publication No. US20050079585A1
; GENERAL INFORMATION:
; APPLICANT: Kolln, Johanna
; APPLICANT: Bredenhorst, Reinhard
; APPLICANT: Spillner, Edzard
; TITLE OF INVENTION: Complement Depletion with Recombinant Human C3 Derivatives
; FILE REFERENCE: P 63782
; CURRENT APPLICATION NUMBER: US/10/884,813
; CURRENT FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1638
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid protein
US-10-884-813-12

Query Match 100.0%; Score 91; DB 5; Length 1638;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWDPGKQLYNVEA 16
|||
Db 1217 KNRWDPGKQLYNVEA 1232

Search completed: May 15, 2006, 16:31:27
Job time : 165 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 16:31:41 ; Search time 28 Seconds
(without alignments)
26.828 Million cell updates/sec

Title: US-09-865-281A-1

Perfect score: 91

Sequence: 1 KNREDPGKQLYNVEA 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 4694837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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12: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	91	100.0	310	9	US-10-921-415-8
3	91	100.0	310	9	US-10-921-415-9
4	91	100.0	1663	9	US-10-982-545-6
5	91	100.0	1663	11	US-11-177-506-34
6	73	80.2	300	8	US-10-514-462-11
7	43	47.3	347	11	US-11-079-463-5775
8	43	47.3	499	9	US-10-514-055-5
9	43	47.3	591	11	US-11-188-298-713
10	43	47.3	591	11	US-11-188-298-8505
11	43	47.3	591	11	US-11-188-298-10639
12	43	47.3	591	11	US-11-188-298-13585
13	43	47.3	655	11	US-11-188-298-1487
14	43	47.3	842	11	US-11-100-356-2
15	43	47.3	847	8	US-10-514-462-1
16	42	46.2	374	9	US-10-517-939-340
17	42	46.2	374	9	US-10-517-939-356
18	40	44.0	189	9	US-10-506-454-336
19	39	42.9	83	9	US-10-934-944-347
20	39	42.9	83	9	US-10-934-944-348
21	39	42.9	83	11	US-11-116-881A-2244

22	39	42.9	83	11	US-11-116-881A-2245	Sequence 2245, Ap
23	39	42.9	191	11	US-11-188-298-11339	Sequence 11339, A
24	39	42.9	250	11	US-11-096-568A-31657	Sequence 31657, A
25	39	42.9	302	11	US-11-096-568A-31656	Sequence 31656, A
26	39	42.9	320	11	US-11-079-463-8514	Sequence 8514, Ap
27	39	42.9	326	11	US-11-024-959-327	Sequence 327, App
28	39	42.9	355	11	US-11-188-298-4023	Sequence 4023, Ap
29	39	42.9	479	9	US-10-517-939-250	Sequence 250, App
30	39	42.9	513	11	US-11-188-298-12438	Sequence 12438, A
31	39	42.9	521	11	US-11-087-089-6169	Sequence 6169, Ap
32	39	42.9	521	11	US-11-188-298-14318	Sequence 14318, A
33	39	42.9	525	9	US-10-934-944-170	Sequence 170, App
34	39	42.9	525	9	US-10-934-944-188	Sequence 188, App
35	39	42.9	525	11	US-11-116-881A-179	Sequence 179, App
36	39	42.9	525	11	US-11-116-881A-197	Sequence 197, App
37	39	42.9	832	11	US-11-108-172-1081	Sequence 1081, Ap
38	39	42.9	958	11	US-11-108-172-1087	Sequence 1087, Ap
39	39	42.9	1128	11	US-11-079-463-9398	Sequence 9398, Ap
40	38.5	42.3	166	11	US-11-079-463-6057	Sequence 6057, Ap
41	38.5	42.3	336	11	US-11-096-568A-7234	Sequence 7234, Ap
42	38.5	42.3	341	11	US-11-096-568A-7233	Sequence 7233, Ap
43	38.5	42.3	355	11	US-11-096-568A-7232	Sequence 7232, Ap
44	38.5	42.3	917	11	US-11-188-298-3936	Sequence 3936, Ap
45	38	41.8	336	11	US-11-129-143-105	Sequence 105, App

ALIGNMENTS

RESULT 1

US-10-921-415-7
; Sequence 7, Application US/10921415
; Publication No. US20060014681A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Xiaojiang
; APPLICANT: Holers, V. Michael
; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND US.
; FILE REFERENCE: 2848-43
; CURRENT APPLICATION NUMBER: US/10/921,415
; CURRENT FILING DATE: 2004-08-16
; PRIOR APPLICATION NUMBER: US/09/834,309
; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-921-415-7

Query Match 100.0%; Score 91; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNREDPGKQLYNVEA 16

Db 224 KNREDPGKQLYNVEA 239

RESULT 2

US-10-921-415-8
; Sequence 8, Application US/10921415
; Publication No. US20060014681A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Xiaojiang
; APPLICANT: Holers, V. Michael
; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND US.
; FILE REFERENCE: 2848-43
; CURRENT APPLICATION NUMBER: US/10/921,415
; CURRENT FILING DATE: 2004-08-16
; PRIOR APPLICATION NUMBER: US/09/834,309

; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-921-415-8

Query Match 100.0%; Score 91; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWDPGKQLYNVEA 16
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DB 224 KNRWDPGKQLYNVEA 239

RESULT 3
US-10-921-415-9
; Sequence 9, Application US/10921415
; Publication No. US20060014681A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Xiaojiang
; APPLICANT: Holers, V. Michael
; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND USE THEREOF
; FILE REFERENCE: 2848-43
; CURRENT APPLICATION NUMBER: US/10/921,415
; CURRENT FILING DATE: 2004-08-16
; PRIOR APPLICATION NUMBER: US/09/834,309
; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-921-415-9

Query Match 100.0%; Score 91; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWDPGKQLYNVEA 16
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DB 224 KNRWDPGKQLYNVEA 239

RESULT 4
US-10-982-545-6
; Sequence 6, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896

; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1663
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: complement component C3 precursor
; NAME/KEY: SIGNAL
; LOCATION: (1)..(23)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (23)..(667)
; OTHER INFORMATION: complement component C3 beta-chain
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (672)..(1663)
; OTHER INFORMATION: complement component C3 alpha-chain
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(748)
; OTHER INFORMATION: C3a anaphylatoxin peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(747)
; OTHER INFORMATION: biomarker peptide M8933.2, C3a anaphylatoxin
; OTHER INFORMATION: desArg peptide
US-10-982-545-6

Query Match 100.0%; Score 91; DB 9; Length 1663;
Best Local Similarity 100.0%; Pred. No. 6.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWDPGKQLYNVEA 16
| | | | | | | | | | | | | | | | | | | | | |
DB 1217 KNRWDPGKQLYNVEA 1232

RESULT 5
US-11-177-506-34
; Sequence 34, Application US/11177506
; Publication No. US20060029956A1
; GENERAL INFORMATION:
; APPLICANT: Beyer, Wayne F.
; APPLICANT: Venetta, Thomas M.
; APPLICANT: Groelke, John W.
; APPLICANT: Blaesus, Rainer H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DETECTION OF OVARIAN DISEASE
; FILE REFERENCE: 46143/294851
; CURRENT APPLICATION NUMBER: US/11/177,506
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: 60/586,856
; PRIOR FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 1663
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-177-506-34

Query Match 100.0%; Score 91; DB 11; Length 1663;
Best Local Similarity 100.0%; Pred. No. 6.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWDPGKQLYNVEA 16
|||||
Db 1217 KNRWDPGKQLYNVEA 1232

RESULT 6

US-10-514-462-11
; Sequence 11, Application US/10514462
; Publication No. US20060088909A1
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Virus-Like Particles, Methods of Preparation, And Immunogenic
; FILE REFERENCE: 050508-2210
; CURRENT APPLICATION NUMBER: US/10/514,462
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: 60/381,557
; PRIOR FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 300
; TYPE: PRT
; ORGANISM: C3d sequence
US-10-514-462-11

Query Match 80.2%; Score 73; DB 8; Length 300;
Best Local Similarity 75.0%; Pred. No. 0.00012; Mismatches 1; Indels 0; Gaps 0;
Matches 12; Conservative 3;

QY 1 KNRWDPGKQLYNVEA 16
:|||||:|||||
Db 197 RNRWEPDQQLYNVEA 212

RESULT 7

US-11-079-463-5775
; Sequence 5775, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FRA
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 5775
; LENGTH: 347
; TYPE: PRT
; ORGANISM: B.fragilis
US-11-079-463-5775

Query Match 47.3%; Score 43; DB 11; Length 347;
Best Local Similarity 63.8%; Pred. No. 14; Mismatches 2; Indels 0; Gaps 0;
Matches 7; Conservative 2;

QY 4 WEDPGKQLYN 14
|||||
Db 295 WEDPKQLSDI 305

RESULT 8

US-10-514-055-5
; Sequence 5, Application US/10514055
; Publication No. US20060073576A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON CORPORATION
; TITLE OF INVENTION: HIV ENVELOPE-CD4 COMPLEXES AND HYBRIDS

; FILE REFERENCE: PPI8701.003 (CHIR-18701/02WO)
; CURRENT APPLICATION NUMBER: US/10/514,055
; CURRENT FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: 60/459,314
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/378,543
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: gpl20.modsf62
; NAME/KEY: MISC_FEATURE
; LOCATION: (127)..(151)
; OTHER INFORMATION: V1 loop
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (152)..(191)
; OTHER INFORMATION: V2 loop
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (291)..(324)
; OTHER INFORMATION: V3 loop
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (378)..(405)
; OTHER INFORMATION: V4 loop
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (447)..(459)
; OTHER INFORMATION: V5 loop
US-10-514-055-5

Query Match 47.3%; Score 43; DB 9; Length 499;
Best Local Similarity 54.5%; Pred. No. 21; Mismatches 6; Conservative 3; Indels 0; Gaps 0;
Matches 6;

QY 2 NRWDPGKQLY 12
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Db 412 NRWQEVGKAMY 422

RESULT 9

US-11-188-298-713
; Sequence 713, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 713
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae TIGR4
US-11-188-298-713

Query Match 47.3%; Score 43; DB 11; Length 591;
Best Local Similarity 46.7%; Pred. No. 25; Mismatches 7; Conservative 4; Indels 0; Gaps 0;
Matches 7;

QY 1 KNRWDPGKQLYNVE 15
|||||
Db 475 RKNYEDTNKHLFGVD 489


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RESULT 15
US-10-514-462-1
; Sequence 1, Application US/10514462
; Publication No. US20060088909A1
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Virus-Like Particles, Methods of Preparation, And Immunogenic
; FILE REFERENCE: 050508-2210
; CURRENT APPLICATION NUMBER: US/10/514,462
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: 60/381,557
; PRIOR FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 847
; TYPE: PRT
; ORGANISM: HIV SF162 Envelope Protein
US-10-514-462-1

Query Match          47.3%; Score 43; DB 8; Length 847;
Best Local Similarity 54.5%; Pred. No. 36;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Db      415 NRQEVGKAWY 425

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Job time : 29 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 16:12:36 ; Search time 38 Seconds
(without alignments)
40.512 Million cell updates/sec

Title: US-09-865-281A-1

Perfect score: 91

Sequence: 1 KNRWDPGKQLYNVEA 16

Scoring table: BLOSUM62

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Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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2	80	87.9	1663	1 C3RT	complement C3 prec
3	79	86.8	726	2 A27602	complement C3 - ra
4	73	80.2	1663	1 C3MS	complement C3 prec
5	58	63.7	1666	1 C3GP	complement C3 prec
6	52	57.1	1358	2 B86241	hypothetical prote
7	44.5	48.9	490	2 D71401	probable selenium-
8	44	48.4	590	2 A44068	cell pattern forma
9	43	47.3	78	2 G82153	hypothetical prote
10	43	47.3	432	2 T05236	hypothetical prote
11	43	47.3	591	2 B97952	pyruvate oxidase (
12	43	47.3	591	2 F95084	pyruvate oxidase [
13	43	47.3	852	2 T12016	envelope glycoprot
14	43	47.3	1651	1 C3NJ	complement C3 prec
15	42.5	46.7	537	2 B90598	ABC transporter at
16	42	46.2	923	2 E83574	hypothetical prote
17	41	45.1	359	2 S45700	G-alpha-11 protein
18	41	45.1	538	2 E85438	step II splicing f
19	41	45.1	574	2 T16230	hypothetical prote
20	41	45.1	2166	2 G70163	hypothetical prote
21	41	45.1	5138	2 B96695	hypothetical prote
22	40.5	44.5	400	1 JCI428	ketol-acid reducto
23	40	44.0	166	2 A85077	hypothetical prote
24	40	44.0	274	2 S75320	hypothetical prote
25	40	44.0	290	2 G82360	diaminopimelate ep
26	40	44.0	311	2 C89894	methionyl-tRNA for
27	40	44.0	331	2 AI2972	two component sens
28	40	44.0	331	2 B98310	probable transmemb
29	40	44.0	359	1 RGHUGY	GTP-binding regula

RESULT 1

C3HU

complement C3 precursor [validated] - human

N:Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit;

C:Species: Homo sapiens (man)

C>Date: 28-Aug-1985 #sequence revision 28-Aug-1985 #text change 09-Jul-2004

C:Accession: A94065; A37999; A92187; A27603; A23435; A45830; B45830; A01257; A01258

R:de Bruijn, M.H.L.; Fey, G.H. 82, 708-712, 1985

Proc. Natl. Acad. Sci. U.S.A. 82, 708-712, 1985

A:Title: Human complement component C3: cDNA coding sequence and derived primary structu

A:Reference number: A94065; MUID:85140166; PMID:2579379

A:Accession: A94065

A:Molecule type: mRNA

A:Residues: 1-1663 <DEB>

A:Cross-references: UNIPROT:P01024; UNIPARC:UPI0000047168; GB:K02765; NID:g179664; PIDN

R:Vik, D.P.; Amiguet, P.; Moffat, G.J.; Fey, M.; Amiguet-Barra, F.; Wetzel, R.A.; Tack,

Biochemistry 30, 1080-1085, 1991

A:Title: Structural features of the human C3 gene: intron/exon organization, transcript

A:Reference number: A37999; MUID:91113687; PMID:1703437

A:Contents: intron/exon structure of gene

A:Accession: A37999

A:Molecule type: DNA

A:Residues: 1-25 <VIK>

A:Cross-references: UNIPARC:UPI0000173214; GB:M63423

A:Note: the authors translated the codon GGT for residue 6 as Leu, CCC for residue 7 as

R:Hugli, T.E. 250, 8293-8301, 1975

J. Biol. Chem. 250, 8293-8301, 1975

A:Title: Human anaphylatoxin (C3a) from the third component of complement.

A:Reference number: A92187; MUID:76069169; PMID:1238393

A:Accession: A92187

A:Molecule type: protein

A:Residues: 672-680, 'N', 682-699, 'Q', 701-748 <HUG>

A:Cross-references: UNIPARC:UPI0000150417

R:Daoudaki, M.E.; Becherer, J.D.; Lambiris, J.D.

J. Immunol. 140, 1577-1580, 1988

A:Title: A 34-amino acid peptide of the third component of complement mediates properdi

A:Reference number: A27603; MUID:88154452; PMID:3279119

A:Accession: A27603

A:Molecule type: protein

A:Residues: 1409-1563 <DAO>

A:Cross-references: UNIPARC:UPI0000173215

R:Hellman, U.; Eggertsen, G.; Engstrom, A.; Sjoquist, J.

Biochem. J. 230, 353-361, 1985

A:Title: Amino acid sequence of the trypsin-generated C3d fragment from human complement

A:Reference number: A23435; MUID:86025442; PMID:3876831

A:Accession: A23435

A:Molecule type: protein

A:Residues: 1002-1012, 'E', 1014-1303 <HEL>

A:Cross-references: UNIPARC:UPI0000173216

A:Note: sequence corresponding to residues 1072-1100 was not determined but was taken fr

R:Poznansky, M.C.; Clissold, P.M.; Lachmann, P.J.

J. Immunol. 143, 1254-1258, 1989

ALIGNMENTS

hypothetical prote
hypothetical prote
polygalacturonase
probable htpG prot
hypothetical prote
hypothetical prote
diaminopimelate ep
protein F16A14.8 [l
lipoprotein [impor
ABC transporter pe
hypothetical prote
hypothetical prote
probable galactosi
chitinase (EC 3.2.
phenylalanine-tRNA
hypothetical prote

A;Title: The difference between human C3F and C3S results from a single amino acid change 3.

A;Reference number: A45830; MUID:89309808; PMID:2473125

A;Accession: A45830

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1212-1215, 'N', 1217-1223 <POZ>

A;Cross-references: UNIPARC:UPI0000173217

A;Note: this is the C3S allele

A;Accession: B45830

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1212-1223 <POZ>

A;Cross-references: UNIPARC:UPI0000173218

R;Dolmer, K.; Sottrup-Jensen, L.
FEBS Lett. 315, 85-90, 1993

A;Title: Disulfide bridges in human complement component C3b.

A;Reference number: S27041; MUID:93106233; PMID:8416818

A;Contents: annotation; disulfide bonds

C;Comment: The sequence shown is the C3 fast (C3F) allele, which is found mainly in Caucasian. Complement C3 contains two chains, formed by removal of four residues and of the alternative complement pathways, releases the C3a anaphylatoxin from the amino end of the native-complement-pathway C3/C5 convertase.

C;Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.

C;Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign particles. The activity of C3b is regulated by proteolytic cleavage.

C;Comment: The major site of synthesis of this plasma protein is the liver.

C;Genetics:

A;Gene: GDB:3

A;Cross-references: GDB:119044; OMIM:120700

A;Map position: 19p13.3-19p13.3

A;Note: contains 41 exons

C;Superfamily: alpha-2-macroglobulin

C;Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein; F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-667/Product: complement C3 and C3b beta chain #status predicted <C3BB>

F;23-667,672-1663/Product: complement C3 #status predicted <CC3>

F;23-667,749-1663/Product: C3b #status predicted <C3B>

F;672-1663/Product: complement C3 alpha chain #status predicted <CC3A>

F;672-748/Product: C3a anaphylatoxin #status predicted <C3T>

F;749-1663/Product: C3b alpha' chain #status predicted <C3BA>

F;946-1303/Product: C3dk fragment #status predicted <CDK>

F;955-1303/Product: C3dg fragment #status predicted <CDG>

F;955-1001/Product: C3g fragment #status predicted <C3G>

F;1002-1303/Product: C3d fragment #status experimental <C3D>

F;1424-1457/Region: propeptide binding

F;85,939/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;559-816,827-862,693-720,694-727,707-728,873-1513,1101-1158,1358-1489,1399-1458,1506-1513/Binding site: Arg-Ser (C3 convertase) #status predicted

F;748-749/Cleavage site: Arg-Glu (complement factor I) #status predicted

F;954-955/Cleavage site: Arg-Glu (complement factor I) #status predicted

F;1010-1013/Cross-link: thiolester (Cys-Gln) #status experimental

F;1303-1304/Cleavage site: Arg-Ser (complement factor I) #status predicted

F;1320-1321/Cleavage site: Arg-Ser (complement factor I) #status predicted

F;1617/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 91; DB 1; Length 1663;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNWEDPGKQLYNVEA 16
Db 1217 KNWEDPGKQLYNVEA 1232

RESULT 2

C3RT

N;Alternate names: 37K phospholipase A2 inhibitory protein

N;Contents: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit; C;Species: Rattus norvegicus (Norway rat)

C;Date: 04-Dec-1992 #sequence revision 07-Oct-1994 #text change 09-Jul-2004

C;Accession: S15764; A54562; A01260; B35979; A35979; PNO567; PNO566; A32281; S08692

R;Maumli, Y.; Sobda, M.; Ikehara, Y.

F:25-566/Product: complement C3 and C3b beta chain #status predicted <C3BB>
 F:25-566, 671-1663/Product: complement C3 #status predicted <CC3>
 F:25-566, 749-1663/Product: complement C3b #status predicted <C3B>
 F:671-1663/Product: complement C3 alpha chain #status predicted <C3A>
 F:671-748/Product: C3a anaphylatoxin #status experimental <C3T>
 F:749-1663/Product: complement C3b alpha' chain #status predicted <C3BA>
 F:946-1303/Product: C3dk fragment #status predicted <CDK>
 F:1002-1303/Product: C3d fragment #status predicted <C3D>
 F:1424-1457/Region: properdin binding
 F:558-816, 626-661, 693-720, 694-727, 707-728, 873-1513, 1101-1158, 1358-1489, 1389-1458, 1506-1513
 F:748-749/Cleavage site: Arg-Ser (C3 convertase) #status predicted
 F:939, 1617/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:1010-1013/Cross-link: thioester (Cys-Gln) #status predicted
 F:1303-1304/Cleavage site: Arg-Ser (complement factor I) #status predicted
 F:1320-1321/Cleavage site: Arg-Ser (complement factor I) #status predicted

Query Match 87.9%; Score 80; DB 1; Length 1663;
 Best Local Similarity 81.2%; Pred. No. 0.00012;
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKOLYNVEA 16
 :||||:||||:|||||
 Db 1217 RNRWEPGGQLYNVEA 1232

RESULT 3
 A27602
 complement C3 - rabbit (fragment)
 N:Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit;
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 15-Dec-1988 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
 C:Accession: A27602
 R:Kusano, M.; Choi, N.H.; Tomita, M.; Yamamoto, K.; Migita, S.; Sekiya, T.; Nishimura, S.
 Immunol. Invest. 15, 365-378, 1986
 A:Title: Nucleotide sequence of cDNA and derived amino acid sequence of rabbit complement C3
 A:Reference number: A27602; MUID:87006907; PMID:3019881
 A:Accession: A27602
 A:Molecule type: mRNA
 A:Residues: 1-726 <NUS>
 A:Cross-references: UNIPROT:P12247; UNIPARC:UPI0000127CAD; GB:M32434; NID:G164862; PIDN:
 C:Comment: Complement C3 contains two chains, formed by removal of four residues and lin
 alternative complement pathways, releases the C3a anaphylatoxin from the amino end of b
 native-complement-pathway C3/C5 convertase.
 C:Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.
 C:Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign pa
 e classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by pro
 C:Comment: The major site of synthesis of this plasma protein is the liver.
 C:Superfamily: alpha-2-macroglobulin
 C:Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein;

Query Match 86.8%; Score 79; DB 2; Length 726;
 Best Local Similarity 81.2%; Pred. No. 7.5e-05;
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKOLYNVEA 16
 :||||:||||:|||||
 Db 280 KNRWEPGGQLYNVEA 295

RESULT 4
 C3MS
 complement C3 precursor - mouse
 N:Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit;
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
 C:Accession: A92459; B92459; A92460; A93938; A21898; A54561; S16369; S16189; I49563; I49
 R:Lundwall, A.; Wetzel, R.A.; Domdey, H.; Tack, B.F.; Fey, G.H.
 J. Biol. Chem. 259, 13851-13856, 1984
 A:Title: Structure of murine complement component C3: I. Nucleotide sequence of cloned c
 A:Reference number: A92459; MUID:85054818; PMID:6548745
 A:Accession: A92459
 A:Molecule type: mRNA
 A:Residues: 1-724 <LU1>

A:Cross-references: UNIPROT:P01027; UNIPARC:UPI0000173219
 A:Accession: B92459
 A:Molecule type: DNA
 A:Residues: 1-124 <LU2>
 A:Cross-references: UNIPARC:UPI000017321A
 R:Wetzel, R.A.; Lundwall, A.; Davidson, F.; Gibson, T.; Tack, B.F.; Fey, G.H.
 J. Biol. Chem. 259, 13857-13862, 1984
 A:Title: Structure of murine complement component C3: II. Nucleotide sequence of cloned
 A:Reference number: A92460; MUID:85054819; PMID:6094532
 A:Accession: A92460
 A:Molecule type: mRNA
 A:Residues: 671-1663 <WET>
 A:Cross-references: UNIPARC:UPI000017321B
 R:Domdey, H.; Wiebauer, K.; Kazmaier, M.; Muller, V.; Odink, K.; Fey, G.
 Proc. Natl. Acad. Sci. U.S.A. 79, 7619-7623, 1982
 A:Title: Characterization of the mRNA and cloned cDNA specifying the third component of
 A:Reference number: A93938; MUID:83117730; PMID:6961437
 A:Contents: C3a
 A:Accession: A93938
 A:Molecule type: mRNA
 A:Residues: 671-748 <DOM>
 A:Cross-references: UNIPARC:UPI0000150419
 R:Sottstrup-Jensen, L.; Stepanik, T.M.; Kristensen, T.; Lonblad, P.B.; Jones, C.M.; Wierzb
 Proc. Natl. Acad. Sci. U.S.A. 82, 9-13, 1985
 A:Title: Common evolutionary origin of alpha2-macroglobulin and complement components C3
 A:Reference number: A21898; MUID:85113177; PMID:2578664
 A:Accession: A21898
 A:Molecule type: mRNA
 A:Residues: 25-1663 <SOT>
 A:Cross-references: UNIPARC:UPI000017321C
 R:Hamada, J.; Cavanaugh, P.G.; Miki, K.; Nicolson, G.L.
 Cancer Res. 53, 4418-4423, 1993
 A:Title: A paracrine migration-stimulating factor for metastatic tumor cells secreted by
 A:Reference number: A54561; MUID:93373334; PMID:8364938
 A:Accession: A54561
 A:Molecule type: protein
 A:Residues: 25-41/749-760 <HAM>
 A:Cross-references: UNIPARC:UPI000017321D; UNIPARC:UPI000017321E
 R:Sato, T.; Hong, M.H.; Jin, C.H.; Ishimi, Y.; Udagawa, N.; Shinki, T.; Abe, E.; Suda,
 FBS Lett. 285, 21-24, 1991
 A:Title: The specific production of the third component of complement by osteoblastic c
 A:Reference number: S16189; MUID:91293304; PMID:2065778
 A:Accession: S16369
 A:Molecule type: protein
 A:Residues: 25-31 <SAT>
 A:Cross-references: UNIPARC:UPI000017321F
 A:Accession: S16189
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 671-677, 'X', 679-680 <SA2>
 A:Cross-references: UNIPARC:UPI000017321F
 R:Fey, G.; Domdey, H.; Wiebauer, K.; Whitehead, A.S.; Odink, K.
 Springer Semin. Immunopathol. 6, 119-147, 1983
 A:Title: Structure and expression of the C3 gene.
 A:Reference number: I49563; MUID:84045280; PMID:6356427
 A:Accession: I49563
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 25-136, 'Q', 138-240 <FEY>
 A:Cross-references: UNIPARC:UPI000006D15; GB:M35659; NID:G192280; PIDN:AAA37339.1; PID
 R:Fey, G.H.; Wiebauer, K.; Domdey, H.
 Ann. N. Y. Acad. Sci. 421, 307-312, 1983
 A:Title: Amino acid sequences of mouse complement C3 derived from nucleotide sequences
 A:Reference number: I49576; MUID:84201365; PMID:6609661
 A:Accession: I49576
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 658-761 <RES>
 A:Cross-references: UNIPARC:UPI000016CC86; GB:M33032; NID:G192391; PIDN:AAA37378.1; PID
 C:Comment: Complement C3 contains two chains, formed by removal of four residues and lin
 alternative complement pathways, releases the C3a anaphylatoxin from the amino end of
 native-complement-pathway C3/C5 convertase.

C;Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.
 C;Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign particles and activates the classical complement pathway C3/C5 convertase. The activity of C3b is regulated by protein C and C3b inactivator (C3bI).
 C;Comment: The major site of synthesis of this plasma protein is the liver.
 C;Genetics: 27/2; 90/3
 A;Introns: 27/2; 90/3
 A;Note: the list of introns may be incomplete
 C;Superfamily: alpha-2-macroglobulin
 C;Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein; acute phase reactant; complement pathway C3/C5 convertase.
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-666/Product: complement C3 and C3b beta chain #status predicted <C3BB>
 F;25-666,671-1663/Product: complement C3 #status predicted <CC3>
 F;25-666,749-1663/Product: complement C3b #status predicted <C3b>
 F;25-666,749-1663/Product: complement C3 alpha chain #status predicted <CC3A>
 F;671-1663/Product: complement C3a anaphylatoxin #status predicted <C3T>
 F;749-1663/Product: C3b alpha' chain #status predicted <C3BA>
 F;946-1303/Product: C3dk fragment #status predicted <CDK>
 F;1002-1303/Product: C3d fragment #status predicted <C3D>
 F;1424-1457/Region: properdin binding
 F;559-816,626-661,693-720,694-727,707-728,873-1513,1101-1158,1358-1489,1389-1458,1506-1513/Region: C3 convertase site: Arg-Ser (C3 convertase) #status predicted
 F;748-749/Cleavage site: Arg-Ser (C3 convertase) #status predicted
 F;939,1617/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;1010-1013/Cross-link: thiolester (Cys-Gln) #status predicted
 F;1303-1304/Cleavage site: Arg-Ser (complement factor I) #status predicted
 F;1320-1321/Cleavage site: Arg-Ser (complement factor I) #status predicted
 F;1320-1321/Cleavage site: Arg-Ser (complement factor I) #status predicted
 Query Match 80.2%; Score 73; DB 1; Length 1663;
 Best Local Similarity 75.0%; Pred. No. 0.0017;
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KNRWDPGKOLYNVEA 16
 :|||||:|||||
 Db 1217 RNRWBPQQOLYNVEA 1232
 RESULT 5
 C3GP
 N;Contains: complement C3 precursor - guinea pig
 C;Species: Cavia porcellus (guinea pig)
 C;Date: 07-Feb-1992 #sequence revision 07-Oct-1994 #text change 09-Jul-2004
 C;Accession: A37156; S03375; A20342; D20342; C20342; A31222
 R;Auerbach, H.S.; Burger, R.; Dodds, A.; Colten, H.R.
 J. Clin. Invest. 86, 96-106, 1990
 A;Title: Molecular basis of complement C3 deficiency in guinea pigs.
 A;Reference number: A37156; MUID:90307998; PMID:1973176
 A;Accession: A37156
 A;Molecule type: mRNA
 A;Residues: 1-1666 <AUE>
 A;Cross-references: UNIPROT:P12387; UNIPARC:UPI0000127C48; GB:M34054; NID:g191262; PIDN:R;Gerard, N.P.; Lively, M.O.; Gerard, C.
 Protein Seq. Data Anal. 1, 473-478, 1988
 A;Title: Amino acid sequence of guinea pig C3a anaphylatoxin.
 A;Reference number: S03375; MUID:89113342; PMID:3064079
 A;Accession: S03375
 A;Molecule type: protein
 A;Residues: 676-730, 'N', 732-752 <GER>
 A;Cross-references: UNIPARC:UPI0000173224
 A;Experimental source: complement-activated guinea pig serum
 A;Note: form isolated is inactive C3a anaphylatoxin and is missing the carboxyl-terminal
 R;Thomas, M.L.; Tack, B.F.
 Biochemistry 22, 942-947, 1983
 A;Title: Identification and alignment of a thiol ester site in the third component of guinea pig C3.
 A;Reference number: A90479; MUID:83178889; PMID:6838833
 A;Accession: A20342
 A;Molecule type: protein
 A;Residues: 676-687 <TH>
 A;Cross-references: UNIPARC:UPI0000173225
 A;Accession: D20342
 A;Molecule type: protein
 A;Residues: 993-1012, 1014-1017, 'E', 1019-1030, 'Y' <TH2>
 A;Cross-references: UNIPARC:UPI0000173225
 R;Goldberger, G.; Thomas, M.L.; Tack, B.F.; Williams, J.; Colten, H.R.; Abraham, G.N.

J. Biol. Chem. 256, 12617-12619, 1981
 A;Title: NH2-terminal structure and cleavage of guinea pig pro-C3, the precursor of the C3b component of the complement system. The activity of C3b is regulated by protein C and C3b inactivator (C3bI).
 A;Accession: C20342
 A;Molecule type: protein
 A;Residues: 23-38 <GOL>
 A;Cross-references: UNIPARC:UPI0000173227
 C;Comment: Complement C3 contains two chains, formed by removal of four residues and ligation of the amino end of the alpha chain to the amino end of the beta chain.
 C;Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein; acute phase reactant; complement pathway C3/C5 convertase.
 C;Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.
 C;Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign particles and activates the classical complement pathway C3/C5 convertase. The activity of C3b is regulated by protein C and C3b inactivator (C3bI).
 C;Comment: The major site of synthesis of this plasma protein is the liver.
 C;Superfamily: alpha-2-macroglobulin
 C;Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein; acute phase reactant; complement pathway C3/C5 convertase.
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;23-671/Product: complement C3 and C3b beta chain #status predicted <C3BB>
 F;23-671,676-1666/Product: complement C3 #status predicted <CC3>
 F;23-671,754-1666/Product: complement C3b #status predicted <C3b>
 F;676-1666/Product: complement C3 alpha chain #status predicted <CC3A>
 F;676-753/Product: C3a anaphylatoxin #status predicted <C3T>
 F;754-1666/Product: C3b alpha' chain #status predicted <C3BA>
 F;951-1308/Product: C3dk fragment #status predicted <CDK>
 F;1007-1308/Product: C3d fragment #status predicted <C3D>
 F;1429-1461/Region: properdin binding
 F;557-821,630-666,698-725,699-732,712-733,878-1517,1106-1163,1363-1493,1394-1462,1510-1513/Region: C3 convertase site: Arg-Ser (C3 convertase) #status predicted
 F;753-754/Cleavage site: Arg-Ser (C3 convertase) #status predicted
 F;944,1620/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;1015-1018/Cross-link: thiolester (Cys-Gln) #status experimental
 F;1308-1309/Cleavage site: Arg-Ser (complement factor I) #status predicted
 F;1325-1326/Cleavage site: Arg-Ser (complement factor I) #status predicted
 Query Match 63.7%; Score 58; DB 1; Length 1666;
 Best Local Similarity 62.5%; Pred. No. 0.5;
 Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KNRWDPGKOLYNVEA 16
 :|||||:|||||
 Db 1222 KNRWEEAROKLYSVEA 1237
 RESULT 6
 B82241
 hypothetical protein [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence revision 02-Mar-2001 #text change 09-Jul-2004
 C;Accession: B86241
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, R.; Chinn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, R.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: B86241
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1358 <STO>
 A;Cross-references: UNIPROT:Q9SAC6; UNIPARC:UPI00000A10C3; GB:AE005172; NID:g4874272; P;Map position: 1
 Query Match 57.1%; Score 52; DB 2; Length 1358;
 Best Local Similarity 69.2%; Pred. No. 3 9;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 3 RWEDPGKOLYNVE 15
 :|||:|||||

Db 223 RWERKQMYNPE 235

RESULT 7
D71401
probable selenium-binding protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
A:Variety: Columbia
C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C:Accession: D71401
R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
P.; Wedler, H.; Wedler, R.; Wambutt, R.; Weitzengger, T.; Pohl, T.M.; Terry, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; And
C.; Chalwatzis, N.
A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
A:Reference number: A71400; MUID:98121113; PMID:9461215
A:Accession: D71401
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-490 <BEV>
A:Cross-references: UNIPROT:O23264; UNIPARC:UPI0000000E71; GB:Z97335; NID:G2244747; PID:
C:Genetics:
A:Map position: 4COP9-4G3845
C:Superfamily: Caenorhabditis elegans hypothetical protein Y37A1B.5

Query Match 48.9%; Score 44.5; DB 2; Length 490;
Best Local Similarity 56.2%; Pred. No. 22;
Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
QY 1 KNRWEDPG-KQLYNVE 15
|||||
Db 191 KNRWEPGHSLFYGD 206
|||||

RESULT 8
A44068
cell pattern formation-associated protein - Emericella nidulans
N:Alternate names: cell differentiation and spatial organization regulator stuA
C:Species: Emericella nidulans, Aspergillus nidulans
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A44068; S27413
R:Miller, K.Y.; Wu, J.; Miller, B.L.
Genes Dev. 6, 1770-1782, 1992
A:Title: StuA is required for cell pattern formation in Aspergillus.
A:Reference number: A44068; MUID:92387550; PMID:1516832
A:Accession: A44068
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-590 <ML>
A:Cross-references: UNIPROT:P36011; UNIPARC:UPI0000136159; EMBL:M83569; NID:g168095; PID:
A:Note: sequence extracted from NCBI backbone (NCBIP:112625)
C:Genetics:
A:Introns: 92/1; 157/1; 201/2
C:Keywords: DNA binding; nucleus; transcription regulation

Query Match 48.4%; Score 44; DB 2; Length 590;
Best Local Similarity 61.5%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4 WEDPGKQLYNVEA 16
|||||
Db 135 WEDEGSLCYQVEA 147
|||||

RESULT 9
G82153
hypothetical protein VC1802 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: G82153

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Esmolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I.
l., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: G82153
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-78 <HEI>
A:Cross-references: UNIPROT:Q9KR44; UNIPARC:UPI000000C30F3; GB:AE004257; GB:AE003852; NI
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1802
A:Map position: 1

Query Match 47.3%; Score 43; DB 2; Length 78;
Best Local Similarity 87.5%; Pred. No. 5.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 6 DPGKQLYN 13
|||||
Db 11 DPGKQLYN 18
|||||

RESULT 10
T05236
hypothetical protein F18A5.60 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05236
R:Bevan, M.; Weber, N.; Grueninger, D.; Schmidheini, T.; Bancroft, I.; Mewes, H.W.; May,
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15405
A:Accession: T05236
A:Molecule type: DNA
A:Residues: 1-432 <BEV>
A:Cross-references: UNIPROT:Q9SVP5; UNIPARC:UPI00000A22A3; EMBL:AL035528
A:Experimental source: cultivar Columbia; BAC clone F18A5
C:Genetics:
A:Map position: 4
A:Introns: 191/3; 223/3; 274/2; 389/1; 401/3
A:Note: F18A5.60

Query Match 47.3%; Score 43; DB 2; Length 432;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 KNRWEDPGK 9
|||||
Db 348 ENRWEDPSR 356
|||||

RESULT 11
B97952
pyruvate oxidase (EC 1.2.3.3) [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 31-Dec-2004
C:Accession: B97952
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.;
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A:Title: Genome of the Bacterium *Streptococcus pneumoniae* Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: B97952
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-591 <KUR>
A:Cross-references: UNIPROT:Q8DQJ4; UNIPARC:UPI00000E34BC; GB:AE007317; PIDN:AAK99446.1
C:Genetics:
A:Gene: spxB

C;Superfamily: thiamine diphosphate-dependent enzyme, acetolactate synthase type
C;Keywords: oxidoreductase

Query Match 47.3%; Score 43; DB 2; Length 591;

Best Local Similarity 46.7%; Pred. No. 47;

Matches 7; Conservative 4; Mismatches 0; Indels 4; Gaps 0;

Qy 1 KNRWDPGKQLYNVE 15

|||||

Db 475 KNRKYEDTNKHLFGVD 489

RESULT 12

F95084

pyruvate oxidase [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 31-Dec-2004

C;Accession: F95084

R;Tottelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid

on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle,

nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: F95084

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-591 <KUR>

A;Cross-references: UNIPROT:Q54970; UNIPARC:UPI000005156C; GB:A5005672; PIDN:AAK74871.1;

A;Experimental source: strain TIGR4

C;Genetics:

A;Gene: SP0730

C;Superfamily: thiamine diphosphate-dependent enzyme, acetolactate synthase type

Query Match 47.3%; Score 43; DB 2; Length 591;

Best Local Similarity 46.7%; Pred. No. 47;

Matches 7; Conservative 4; Mismatches 0; Indels 4; Gaps 0;

Qy 1 KNRWDPGKQLYNVE 15

|||||

Db 475 KNRKYEDTNKHLFGVD 489

RESULT 13

T12016

envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: T12016

R;McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.

AIDS Res. Hum. Retroviruses 14, 329-337, 1998

A;Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S

A;Reference number: 217379; MUID:98178716; PMID:9519894

A;Accession: T12016

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-852 <MCC>

A;Cross-references: UNIPROT:Q41883; UNIPARC:UPI000010B1F2; EMBL:U90934; NID:G2351783; PT

C;Genetics:

A;Gene: env

C;Superfamily: type E retrovirus env polyprotein

Query Match 47.3%; Score 43; DB 2; Length 852;

Best Local Similarity 54.5%; Pred. No. 70;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLY 12

|||||

Db 421 NRWQEVGKAMY 431

RESULT 14

C3N7

complement C3 precursor - monoclod cobra

N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit;

C;Species: Naja naja kaouthia, Naja naja siamensis (monoclod cobra)

C;Date: 18-Jun-1993 #sequence_revision 07-Oct-1994 #text_change 17-Mar-2000

C;Accession: A46513

R;Frizinger, D.C.; Petrella, E.C.; Connelly, M.B.; Bredehorst, R.; Vogel, C.W.

J. Immunol. 149, 3554-3562, 1992

A;Title: Primary structure of cobra complement component C3.

A;Reference number: A46513; MUID:93056528; PMID:1431125

A;Accession: A46513

A;Molecule type: mRNA

A;Residues: 1-1651 <FRI>

A;Cross-references: UNIPARC:UPI0000127C4B; GB:L02365; NID:G213372; PIDN:AAA49385.1; PID

A;Note: authors' translation shows Arg-1408 after residue 1438 and, consequently, resid

A;Note: sequence extracted from NCBI backbone (NCBIP:118403) and corrected to correspon

C;Comment: Complement C3 contains two chains, formed by removal of four residues and 1 li

alternative complement pathways, releases the C3a anaphylatoxin from the amino end of

native-complement-pathway C3/C5 convertase.

C;Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.

C;Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign p

e classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by p

C;Comment: The major site of synthesis of this plasma protein is the liver.

C;Superfamily: alpha-2-macroglobulin

C;Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-655/Product: complement C3 and C3b beta chain #status predicted <C3BB>

F;23-655,660-1651/Product: complement C3 #status predicted <CC3>

F;23-655,739-1651/Product: complement C3b #status predicted <C3B>

F;660-1651/Product: complement C3 alpha chain #status predicted <CC3A>

F;660-738/Product: C3a anaphylatoxin #status predicted <C3T>

F;739-1651/Product: complement C3b alpha' chain #status predicted <C3BA>

F;7412-1445/Region: properdin binding

F;546-807,615-650,683-710,684-717,697-718,863-1501,1091-1147,1346-1477,1377-1446,1494-1

F;738-739/Cleavage site: Arg-Ser (C3 convertase) #status predicted

F;999-1002/Cross-link: thiolester (Cys-Gln) #status predicted

Query Match 47.3%;

Best Local Similarity 40.0%;

Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KNRWDPGKQLYNVE 15

|||||

Db 1204 RNRWEYNARTNIE 1218

RESULT 15

B90598

ABC transporter atp-binding protein [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C;Species: Mycoplasma pulmonis

C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 05-Oct-2004

C;Accession: B90598

R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.

Nucleic Acids Res. 29, 2145-2153, 2001

A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pul

A;Reference number: A99512; MUID:21267165; PMID:11353084

A;Accession: B90598

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-537 <KUR>

A;Cross-references: UNIPROT:Q98PN2; UNIPARC:UPI000000D4649; GB:AL445566; PID:G14090105;

A;Experimental source: strain UAB CTIP

C;Genetics:

A;Gene: MYPU_6900

A;Genetic code: SGC3

Query Match 46.7%;

Best Local Similarity 56.2%;

Matches 9; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

Qy 3 RWE---DPGKQLYNVE 15

|||||

Db 308 KWEINRVPKGQILNVE 323

Search completed: May 15, 2006, 16:16:59
Job time : 40 secs

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GenCore version 5.1.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 16:08:46 ; Search time 185 Seconds
(without alignments)
38.000 Million cell updates/sec

Title: US-09-865-281A-1

Perfect score: 91

Sequence: 1 KNRWEDPGKQLYNVEA 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	91	100.0	16	4	AAB92360	Miscellan
2	91	100.0	16	6	ABP58217	Immunosti
3	91	100.0	16	8	AD517594	Peptide d
4	91	100.0	16	9	ADV24825	CR2-bindi
5	91	100.0	17	9	ADV24829	Complemen
6	91	100.0	17	9	ADV24828	Complemen
7	91	100.0	17	9	ADV24828	Complemen
8	91	100.0	41	8	ADT92344	Human com
9	91	100.0	63	5	AAB71451	Human C3
10	91	100.0	294	5	AAB74858	Complemen
11	91	100.0	294	5	AAU74866	Complemen
12	91	100.0	294	5	AAU74869	Complemen
13	91	100.0	294	5	AAU74855	Complemen
14	91	100.0	294	5	AAU74862	Complemen
15	91	100.0	294	5	AAU74859	Complemen
16	91	100.0	294	5	AAU74872	Complemen
17	91	100.0	294	5	AAU74873	Complemen
18	91	100.0	294	5	AAU74863	Complemen
19	91	100.0	294	5	AAU74856	Complemen
20	91	100.0	294	5	AAU74880	Complemen
21	91	100.0	294	5	AAU74860	Complemen
22	91	100.0	294	5	AAU74854	Complemen
23	91	100.0	294	5	AAU74865	Complemen
24	91	100.0	294	5	AAU74867	Complemen
					AAU74861	Complemen

25	91	100.0	294	5	AAU74871	Complemen
26	91	100.0	294	5	AAU74868	Complemen
27	91	100.0	294	5	AAU74874	Complemen
28	91	100.0	294	5	AAU74878	Complemen
29	91	100.0	294	5	AAU74879	Complemen
30	91	100.0	294	5	AAU74857	Complemen
31	91	100.0	294	5	AAU74864	Complemen
32	91	100.0	294	5	AAU74870	Complemen
33	91	100.0	294	5	AAU74875	Complemen
34	91	100.0	294	5	AAU74876	Complemen
35	91	100.0	294	5	AAU74877	Complemen
36	91	100.0	294	5	AAU74881	Complemen
37	91	100.0	310	8	ADI05803	Human com
38	91	100.0	310	8	ADI05805	Human C3d
39	91	100.0	310	8	ADI05804	Human C3d
40	91	100.0	349	2	AAR10900	Human pho
41	91	100.0	349	2	AAR21776	Phospholi
42	91	100.0	349	2	AAR51949	Phospholi
43	91	100.0	370	8	ADK72548	Fusion pr
44	91	100.0	383	8	ADK72551	Fusion pr
45	91	100.0	387	8	ADK72549	Fusion pr

ALIGNMENTS

RESULT 1

AAB92360

ID AAB92360 standard; peptide; 16 AA.

XX AC AAB92360;

XX DT 22-JUN-2001 (first entry)

XX DE Miscellaneous peptide SEQ ID NO:1536.

XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200069900-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US013576.

XX PR 17-MAY-1999; 99US-0134406P.

XX PR 10-SEP-1999; 99US-0153406P.

XX PR 15-OCT-1999; 99US-0159783P.

XX PA (CONJ-) CONJUCHEM INC.

XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX DR WPI; 2001-112059/12.

XX PT Modifying and attaching therapeutic peptides to albumin prevents
peptidase degradation, useful for increasing length of in vivo activity.

XX PS Disclosure; Page 707; 733pp; English.

XX CC The present invention describes a modified therapeutic peptide (I)
comprising a therapeutically active amino acid region (III) and a
reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
a less therapeutically active amino acid region (IV), which covalently
bonds with amino/hydroxyl/thiol groups on blood components to form a
peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
XX CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
factors and neurotransmitters, to protect them from peptidase activity in
vivo for the treatment of various disorders. Endogenous therapeutic

CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention

XX
 SQ Sequence 16 AA;

Query Match 100.0%; Score 91; DB 4; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.5e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKQLYNVEA 16
 |||||
 Db 1 KNRWEDPGKQLYNVEA 16

RESULT 2
 ABP58217

ID ABP58217 standard; peptide; 16 AA.

XX AC

XX ABP58217;

XX 21-MAR-2003 (first entry)

XX Immunostimulant C3d peptide.

XX Immunostimulant; C3d; human; fusion protein; tumour; vaccine; adjuvant.

XX Homo sapiens.

XX WO200297041-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-US016651.

XX 29-MAY-2001; 2001US-00865281.

XX (IMMP-) IMPHERON INC.

XX (INNE-) INNEXUS CORP.

XX Kohler H, Morgan C;

XX WPI; 2003-140458/13.

XX Novel fusion protein for use as molecular adjuvant, has an antibody and a
 PT peptide with immunostimulatory, membrane transport or homophilic
 PT activities, connected to the antibody by peptide bonds.

XX Example 1; Page 14; 39pp; English.

XX The present invention provides a fusion protein made up of an antibody
 CC and a peptide having e.g. immunostimulant, membrane transport or
 CC homophilic activity. The peptide is located at a site in the antibody
 CC such that it does not compromise the antigen recognition of the antibody.
 CC In order to enhance its activity, the peptide may be flanked by loop-
 CC forming or conformation-conferring sequences. The present sequence is an
 CC example of a suitable immunostimulatory peptide for use as a fusion
 CC protein component. The peptide is derived from human C3d amino acids 1217
 CC -1232. In examples from the invention, the C3d peptide was affinity cross
 CC -linked to tumour anti-idiotypic and tumour idiotype vaccine antibodies,
 CC significantly enhancing the immune response to the tumour and protecting
 CC against tumour challenge. The vaccination protocol did not include any
 CC adjuvant, such as Freund's adjuvant or keyhole limpet haemocyanin
 CC conjugation, both of which are not permissible by the FDA for human use

XX Sequence 16 AA;

XX Query Match

100.0%; Score 91; DB 6; Length 16;

Best Local Similarity 100.0%; Pred. No. 6.5e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKQLYNVEA 16
 |||||
 Db 1 KNRWEDPGKQLYNVEA 16

RESULT 3
 ADS17594

ID ADS17594 standard; peptide; 16 AA.

XX AC

XX ADS17594;

XX 02-DEC-2004 (first entry)

XX Peptide derived from the C3d peptide and affinity linked to 3H1 antibody.

XX immunostimulatory; membrane transport; homophilic; signaling protein;
 KW caspase; kinase; phosphatase; viral protein; tumour antigen;
 KW nuclear protein; nucleolar protein; DNA synthesis; cytoskeletal protein;
 KW cell proliferation; cytoskeleton; membrane transporter peptide;
 KW Kaposi fibroblast factor; TAT peptide; HIV-1; antenapedia homeodomain;
 KW herpes virus protein VP22; transportan peptide; Alzheimer's disease;
 KW Huntington's disease; Parkinson's disease; C3d; 3H1; monoclonal antibody;
 KW anti-idiotypic antibody; carcino-embryonic antigen; CEA;
 KW anti-idiotypic vaccine; antibody.

XX Synthetic.

XX WO2004078146-A2.

XX 16-SEP-2004.

XX 05-MAR-2004; 2004WO-US006911.

XX 05-MAR-2003; 2003US-0451980P.

XX (INNE-) INNEXUS BIOTECHNOLOGY INC.

XX (IMMP-) IMPHERON INC.

XX Kohler H, Muller S, Brown TL, Zhao Y, Morgan AC;

XX WPI; 2004-653567/63.

XX New compound for regulating normal or infected cell function comprising
 PT an antibody conjugated to a membrane transporter peptide, useful in
 PT preparing a composition for treating or preventing human diseases, e.g.
 PT Alzheimer's disease.

XX Example 1; SEQ ID NO 1; 50pp; English.

XX The specification describes a fusion protein for regulating normal or
 CC infected cell function, comprising an antibody conjugated to a peptide
 CC having immunostimulatory, membrane transport, and homophilic activities.
 CC The antibody is immunospecific for a signaling protein internal cell
 CC consisting of caspases, kinases or phosphatases, an immature viral
 CC protein, a cell-surface or intracellular tumour antigen, a nuclear or
 CC nucleolar protein participating in regulation of DNA synthesis and gene
 CC expression, or a cytoskeletal protein participating in cell proliferation
 CC or cytoskeleton. The peptide portion of the fusion protein is preferably a
 CC membrane transporter peptide that is endogenous to Kaposi fibroblast
 CC factor, TAT proteins of HIV-1, antenapedia homeodomain-derived peptide,
 CC herpes virus protein VP22, or transportan peptide. Fusion protein of the
 CC invention are useful for preparing a composition for treating or
 CC preventing human diseases, e.g., Alzheimer's disease, Huntington's
 CC disease or Parkinson's disease. The present sequence represents a peptide
 CC derived from the C3d region 1217-1232, which was affinity cross-linked
 CC with 3H1 monoclonal antibody to produce fusion proteins of the invention.
 CC 3H1 is a murine anti-idiotypic antibody which mimics the carcino-
 CC embryonic antigen (CEA), and induces anti-CEA antibodies. The resulting
 CC CD3-3H1 fusion protein was used to enhance an anti-idiotypic vaccine.

XX

SQ Sequence 16 AA;
 Query Match 100.0%; Score 91; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.5e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KNRWDPGKQLYNVEA 16
 |||||
 DB 1 KNRWDPGKQLYNVEA 16
 |||||
 RESULT 4
 ADV24825
 ID ADV24825 standard; peptide; 16 AA.
 XX AC
 XX ADV24825;
 DT 24-FEB-2005 (first entry)
 XX DE
 XX CR2-binding complement C3d peptide, SEQ ID NO:2.
 XX DE
 XX Multivalent ligand; cell signaling; diagnostic; decontamination;
 KW autoimmune disease; immune disorder; cancer; neoplasm; cancer metastasis;
 KW immunosuppressive; immunomodulator; cytostatic; complement C3d.
 XX OS
 XX Unidentified.
 XX US2004248801-A1.
 XX PN
 XX PD
 XX 09-DEC-2004.
 XX XX
 XX 22-MAR-2004; 2004US-00806056.
 XX XX
 XX 21-MAR-2000; 2000US-0191014P.
 XX PR
 XX 21-MAR-2001; 2001US-00815296.
 XX PR
 XX 21-MAR-2003; 2003US-0456778P.
 XX XX
 XX (KIES/) KIESSLING L L.
 XX PA (GRIF/) GRIFFITH B R.
 XX PA (GEST/) GESTWICKI J E.
 XX PA (STRO/) STRONG L.
 XX XX
 PI Kiessling LL, Griffith BR, Gestwicki JE, Strong L;
 XX WPI; 2005-046763/05.
 XX XX
 XX Novel multivalent ligand, useful for inducing biological response,
 PT enhancing aggregation of biological particles and enhancing induction of
 PT cellular response.
 XX XX
 XX Example 3; SEQ ID NO 2; 76pp; English.
 XX PS
 XX XX
 CC The invention relates to a multivalent ligand comprising a plurality of
 CC signal recognition elements (SRE), binding recognition elements (BRE) and
 CC functional elements (FE), and which is bonded to a polymeric scaffold.
 CC The SREs are involved, either directly or indirectly, in biological
 CC signaling processes, while the BREs facilitate the binding associated
 CC with the process. Examples of SREs used in the multivalent ligand include
 CC epitopes (especially one characteristic of a cancer cell), antigens,
 CC antibodies or fragments thereof, cell surface receptors, polysaccharides,
 CC nucleic acids or small drug-like compounds, and suitable BREs include
 CC polysaccharides or metal-chelating groups which are optionally bound to
 CC metals. The FE may be a detectable label, a reporter group or an enzyme.
 CC The invention also relates to use of multivalent ligands in a method for
 CC inducing a biological response in a biological system such as a cell or
 CC organism which comprises one or more receptors recognized by an SRE; a
 CC method of enhancing aggregation of biological particles such as cells or
 CC viruses using a multivalent ligand complex which comprises several
 CC recognition elements which each induce aggregation of one or more of the
 CC biological particles; a method for inducing a cellular response or for
 CC enhancing cellular response induction using a multivalent ligand; a
 CC method of generating an assembly of biological macromolecules or
 CC particles by providing a multivalent ligand comprising a molecular

scaffold to which several biological macromolecules or particles are
 attached via BREs, wherein the number, density and spacing of the BREs is
 controlled; and a library of multivalent ligands of the invention, in
 which the members of the libraries vary in the type, number and/or
 relative positioning of recognition elements, the combinations of BREs
 and SREs present, the presence and/or positioning of spacers, the number
 of repeating units or monomers, and the presence, type or number of FEs.
 The invention also discloses pharmaceutical compositions comprising
 multivalent ligands of the invention. The multivalent ligands are useful
 for modulating immune system cell responses to epitopes, thereby
 inhibiting or attenuating autoimmune disorders, and are also useful for
 treating undesired cell proliferation (cancer) and undesired cell
 migration (metastasis). They can be used in diagnostic applications for
 the detection of biological molecules or particles in biological systems,
 and are useful for preventing or inhibiting biofouling or removing
 undesired cells in a selected environment. The present sequence
 represents a complement C3d peptide able to bind complement receptor CR2
 which may be used as a signal in a multivalent ligand for inducing an
 enhanced immune response.
 XX XX
 SQ Sequence 16 AA;
 Query Match 100.0%; Score 91; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.5e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KNRWDPGKQLYNVEA 16
 |||||
 DB 1 KNRWDPGKQLYNVEA 16
 |||||
 RESULT 5
 ADV24829
 ID ADV24829 standard; peptide; 17 AA.
 XX AC
 XX ADV24829;
 XX XX
 XX 24-FEB-2005 (first entry)
 XX DE
 XX Complement C3d derived peptide, SEQ ID NO:6.
 XX KW
 KW Multivalent ligand; cell signaling; diagnostic; decontamination;
 KW autoimmune disease; immune disorder; cancer; neoplasm; cancer metastasis;
 KW immunosuppressive; immunomodulator; cytostatic; complement C3d.
 XX OS
 OS Synthetic.
 OS Unidentified.
 XX XX
 XX Key Location/Qualifiers
 FT Modified-site 17
 FT /note= "The side chain thiol group is attached to the
 FT polymer backbone of the multivalent ligand"
 XX XX
 XX US2004248801-A1.
 XX XX
 XX 09-DEC-2004.
 XX XX
 XX 22-MAR-2004; 2004US-00806056.
 XX XX
 XX 21-MAR-2000; 2000US-0191014P.
 XX PR
 XX 21-MAR-2001; 2001US-00815296.
 XX PR
 XX 21-MAR-2003; 2003US-0456778P.
 XX XX
 XX (KIES/) KIESSLING L L.
 XX PA (GRIF/) GRIFFITH B R.
 XX PA (GEST/) GESTWICKI J E.
 XX PA (STRO/) STRONG L.
 XX XX
 PI Kiessling LL, Griffith BR, Gestwicki JE, Strong L;
 XX WPI; 2005-046763/05.
 XX XX
 XX Novel multivalent ligand, useful for inducing biological response,
 PT

Query Match 100.0%; Score 91; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKQLYNVEA 16
|||||
DB 2 KNRWEDPGKQLYNVEA 17
|||||

RESULT 7
ADT92344
ID ADT92344 standard; peptide; 41 AA.
XX AC ADT92344;
XX DT 13-JAN-2005 (first entry)
XX DE Human complement C3 peptide, a marker for colorectal cancer Seq 40.
XX colorectal cancer; quantitative detection assay; protein chip technology;
KW mass spectrometry; cell proliferation; complement C3.
XX OS Homo sapiens.
XX PN WO2004090550-A2.
XX PD 21-OCT-2004.
XX PF 07-APR-2004; 2004WO-DK000263.
XX PR 08-APR-2003; 2003DK-00000541.
XX PR 16-JUL-2003; 2003DK-00001085.
XX PA (COLO-) COLOTECH AS.
XX PA (RASK/) RASKOV H H.
XX PI Raskov HH, Albrethsen J, Gammeltoft S, Bogebo RM;
XX WPI; 2004-766501/75.
XX DR
XX DT
XX PT Diagnosing colorectal cancer in sample from mammal, involves use of
XX marker polypeptides having specific molecular weights and degradation
XX product of human serum albumin.
XX Example 19; SEQ ID NO 40; 132pp; English.

XX This invention relates to a novel method for diagnosing human colorectal
XX cancer using novel protein markers. Specifically, it refers to a
XX quantitative detection assay that uses at least one marker chosen from
XX polypeptides having apparent molecular weights ranging between 1005Da and
XX 56800Da, and compares the signal intensity of the marker against a
XX reference value from a healthy person. As such, the present invention
XX describes a method that can be used to diagnose persons with colorectal
XX cancer by means of protein chip technology using mass spectrometry, by
XX identifying differential expression of markers that are indicative of
XX cell proliferation. Preferred protein markers include alpha-fibrinogen
XX protein and human serum albumin where a preferred kit enables detection
XX of a combination of two or more proteins. Accordingly, this method is
XX useful for diagnosing colorectal cancer, as well as predicting clinical
XX outcomes, complications and mortality of an individual already diagnosed
XX with the disease. This peptide sequence is a human complement C3 peptide,
XX an down-regulated blood protein marker for colorectal cancer given in an
XX exemplification of the invention.

XX Sequence 41 AA;
Query Match 100.0%; Score 91; DB 8; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKQLYNVEA 16
|||||

DB 14 KNRWEDPGKQLYNVEA 29
RESULT 8
AAB71451
ID AAB71451 standard; peptide; 63 AA.
XX AC AAB71451;
XX DT 11-DEC-2002 (first entry)
XX DE Human C3 discontinuous Factor H binding site SEQ ID 20.

XX CVF1; cobra venom factor; proCVF1; cobra; antirheumatic; antiarthritic;
KW dermatological; immunosuppressive; vasotropic; vulnary; septic shock;
KW antiinflammatory; antibacterial; decompensation; rheumatoid arthritis;
KW ischaemia-reperfusion injury; thermal injury; lupus erythematosus;
KW respiratory distress syndrome; tissue rejection; complement; tumour;
KW xenotransplantation; gene therapy; burn; cancer.

XX OS Homo sapiens.
XX PN US2002103346-A1.
XX PD 01-AUG-2002.
XX PF 10-AUG-2001; 2001US-00925442.
XX PR 14-JUN-1996; 96US-00662227.
XX PR 03-FEB-1998; 98US-00017947.
XX PA (GEU) UNIV GEORGETOWN.

XX PI Vogel C, Bredehorst R, Fritzing D, Kock M;
XX WPI; 2002-690629/74.

XX Novel recombinant pro-cobra venom factor polypeptide useful for
XX decompensation of animal suffering from septic shock, ischemia-
XX reperfusion injury, arthritis, respiratory distress syndrome, or tissue
XX rejection.

XX Example; Fig 7B; 82pp; English.

XX This invention describes a novel recombinant pro-cobra venom factor
XX polypeptide which has antirheumatic, antiarthritic, dermatological,
XX immunosuppressive, vasotropic, vulnary, antiinflammatory, antibacterial
XX and cytostatic activity. The polypeptide of the invention is useful for
XX decompensation by administering procvf to an animal such as reptile,
XX fish, bird or mammal such as guinea pigs, mice, rats, pigs, baboons,
XX chimps, dogs, cats, horses, cows or humans, suffering from septic shock,
XX ischaemia-reperfusion injury, thermal injury, arthritis, lupus, septic
XX respiratory distress syndrome, or a tissue rejection. Procvf is useful as
XX research agent to deplete the complement activity in the plasma of
XX laboratory animals in vitro and in vivo, as therapeutic agent in humans
XX for treating cancer, for antibody targeting to tumour cells, for
XX depleting complement in patients undergoing xenotransplantation to
XX suppress the hyperacute rejection of the foreign organ, for temporary
XX depletion of complement in patient undergoing gene therapy using
XX retroviral vectors, and for treating diseases with circulating immune
XX complexes e.g. rheumatoid arthritis, lupus erythematosus, septic shock,
XX adult respiratory distress syndrome, ischaemic-reperfusion injury and
XX thermal injury from burns. This sequence represents a fragment of protein
XX described in the disclosure of the invention

XX SQ Sequence 63 AA;

Query Match 100.0%; Score 91; DB 5; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKQLYNVEA 16
|||||

AAU74866	AAU74866 standard; protein; 294 AA.
ID	AAU74866
XX	AAU74866;
XX	09-APR-2002 (first entry)
DT	
XX	Complement pathway protein C3d, N98A mutant.
DE	
XX	Complement; receptor; CD21; CD2; C3d; immune response; B cell stimulator;
KW	vaccine; CD21/CD19 complex; tumour; cancer; mutant; mutein.
KW	
XX	Homo sapiens.
OS	Synthetic.
OS	
XX	
XX	Key Location/Qualifiers
PH	Misc-difference 98
FT	/note= "wild type Asn substituted by Ala"
FT	
XX	W0200192295-A2..
PN	
XX	06-DEC-2001..
PD	
XX	30-MAY-2001; 2001WO-CA0000785.
PF	
XX	30-MAY-2000; 2000US-0207434P.
PR	
XX	(UTOR) UNIV TORONTO.
PA	
XX	Iserman DE, Clemenza L;
PI	
XX	WPI; 2002-114323/15.
DR	
XX	Ligand useful for modulating immune response such as in the preparation
PT	of vaccine comprises CD21 contacting amino acid residues of C3d molecule.
PT	
XX	Disclosure; Page; 53pp; English.
XX	
XX	The invention describes a ligand of the complement receptor 2 (CD21 or
CC	CD2) comprising amino acid residues 36-39 and 160-167 of the C3d
CC	molecule. The ligand is useful in the manufacture of a medicament such as
CC	a vaccine for modulating the immune response of a host (preferably tumour
CC	cells), and as antigens in immunogenic compositions, therapeutics
CC	diagnostic reagents, in the generation of diagnostic agents and as cancer
CC	therapeutics. The ligand has the ability to bind CD21 and stimulate B
CC	cells through the CD21/CD19 complex. Non-naturally occurring ligands and
CC	site specific mutated analogues of C3d demonstrate an enhanced binding
CC	affinity for CD21 as compared to the binding affinity of a wild-type C3d
CC	molecule. The ligand alters the immunogenicity of an antigen, e.g. by
CC	inducing or enhancing an immune response to an antigen in a host and thus
CC	protects the host against disease caused by the pathogen. This sequence
CC	represents the complement pathway protein C3d N98A mutant, used to study
CC	the interaction of C3d with complement receptor 2 (CD21/CD2), described
CC	in the method of the invention. Note: This sequence does not appear in
CC	the specification but has been created from a C3d wild type sequence
CC	referenced on page 11 of the invention
XX	
XX	Sequence 294 AA;
XX	
XX	Query Match 100.0%; Score 91; DB 5; Length 294;
XX	Best Local Similarity 100.0%; Pred. No. 1.2e-05;
XX	Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Oy	1 KNRWDPGKOLYNVEA 16
Db	224 KNRWDPGKOLYNVEA 239
RESULT 11	
AAU74869	
ID	AAU74869 standard; protein; 294 AA.
XX	
AC	AAU74869;


```

XX 09-APR-2002 (first entry)
XX Complement pathway protein C3d, D163A mutant.
DE
KW Complement; receptor; CD21; CD2; C3d; immune response; B cell stimulator;
KW vaccine; CD21/CD19 complex; tumour; cancer; mutant; mutein.
XX
OS Homo sapiens.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 163
FT /note= "Wild type Asp substituted by Ala"
XX
XX WO200192295-A2.
XX
XX 06-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-CA000785.
XX
XX 30-MAY-2000; 2000US-0207434P.
XX
XX (UTOR ) UNIV TORONTO.
XX
XX Iserman DE, Clemenza L;
XX WPI; 2002-114323/15.
XX
XX Ligand useful for modulating immune response such as in the preparation
XX of vaccine comprises CD21 contacting amino acid residues of C3d molecule.
XX
XX Disclosure; Page; 53pp; English.
XX
XX The invention describes a ligand of the complement receptor 2 (CD21 or
XX CD2) comprising amino acid residues 36-39 and 160-167 of the C3d
XX molecule. The ligand is useful in the manufacture of a medicament such as
XX a vaccine for modulating the immune response of a host (preferably tumour
XX vaccine), and as antigens in immunogenic compositions, therapeutics
XX diagnostic reagents, in the generation of diagnostic agents and as cancer
XX therapeutics. The ligand has the ability to bind CD21 and stimulate B
XX cells through the CD21/CD19 complex. Non-naturally occurring ligands and
XX site specific mutated analogues of C3d demonstrate an enhanced binding
XX affinity for CD21 as compared to the binding affinity of a wild-type C3d
XX molecule. The ligand alters the immunogenicity of an antigen, e.g. by
XX inducing or enhancing an immune response to an antigen in a host and thus
XX protects the host against disease caused by the pathogen. This sequence
XX represents the complement pathway protein C3d D163A mutant, used to study
XX the interaction of C3d with complement receptor 2 (CD21/CD2), described
XX in the method of the invention. Note: This sequence does not appear in
XX the specification but has been created from a C3d wild type sequence
XX referenced on page 11 of the invention
XX
XX Sequence 294 AA;
XX
XX Query Match 100.0%; Score 91; DB 5; Length 294;
XX Best Local Similarity 100.0%; Pred. No. 1.2e-05;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 KNRWDPGKQLYNVEA 16
DB 224 KNRWDPGKQLYNVEA 239
|||||
RESULT 12
AAU74855
ID AAU74855 standard; protein; 294 AA.
XX
XX AAU74855;
XX
XX 09-APR-2002 (first entry)
XX Complement pathway protein C3d, E37A mutant.

```

```

XX Complement; receptor; CD21; CD2; C3d; immune response; B cell stimulator;
KW vaccine; CD21/CD19 complex; tumour; cancer; mutant; mutein.
XX
XX Homo sapiens.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 37
FT /note= "Wild type Glu substituted by Ala"
XX
XX WO200192295-A2.
XX
XX 06-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-CA000785.
XX
XX 30-MAY-2000; 2000US-0207434P.
XX
XX (UTOR ) UNIV TORONTO.
XX
XX Iserman DE, Clemenza L;
XX WPI; 2002-114323/15.
XX
XX Ligand useful for modulating immune response such as in the preparation
XX of vaccine comprises CD21 contacting amino acid residues of C3d molecule.
XX
XX Disclosure; Page; 53pp; English.
XX
XX The invention describes a ligand of the complement receptor 2 (CD21 or
XX CD2) comprising amino acid residues 36-39 and 160-167 of the C3d
XX molecule. The ligand is useful in the manufacture of a medicament such as
XX a vaccine for modulating the immune response of a host (preferably tumour
XX vaccine), and as antigens in immunogenic compositions, therapeutics
XX diagnostic reagents, in the generation of diagnostic agents and as cancer
XX therapeutics. The ligand has the ability to bind CD21 and stimulate B
XX cells through the CD21/CD19 complex. Non-naturally occurring ligands and
XX site specific mutated analogues of C3d demonstrate an enhanced binding
XX affinity for CD21 as compared to the binding affinity of a wild-type C3d
XX molecule. The ligand alters the immunogenicity of an antigen, e.g. by
XX inducing or enhancing an immune response to an antigen in a host and thus
XX protects the host against disease caused by the pathogen. This sequence
XX represents the complement pathway protein C3d E37A mutant, used to study
XX the interaction of C3d with complement receptor 2 (CD21/CD2), described
XX in the method of the invention. Note: This sequence does not appear in
XX the specification but has been created from a C3d wild type sequence
XX referenced on page 11 of the invention
XX
XX Sequence 294 AA;
XX
XX Query Match 100.0%; Score 91; DB 5; Length 294;
XX Best Local Similarity 100.0%; Pred. No. 1.2e-05;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 KNRWDPGKQLYNVEA 16
DB 224 KNRWDPGKQLYNVEA 239
|||||
RESULT 13
AAU74862
ID AAU74862 standard; protein; 294 AA.
XX
XX AAU74862;
XX
XX 09-APR-2002 (first entry)
XX Complement pathway protein C3d, E37A/E39A mutant.
XX
XX Complement; receptor; CD21; CD2; C3d; immune response; B cell stimulator;
KW vaccine; CD21/CD19 complex; tumour; cancer; mutant; mutein.
XX

```

```

OS Homo sapiens.
OS Synthetic.
XX
XX
XX Key Location/Qualifiers
XX Misc-difference 37
XX /note= "Wild type Glu substituted by Ala"
XX
XX Misc-difference 39
XX /note= "Wild type Glu substituted by Ala"
XX
XX
XX WO200192295-A2.
XX
XX 06-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-CA000785.
XX
XX 30-MAY-2000; 2000US-0207434P.
XX
XX (UTOR ) UNIV TORONTO.
XX
XX Isenman DE, Clemenza L;
XX WPI; 2002-114323/15.
XX
XX Ligand useful for modulating immune response such as in the preparation
XX of vaccine comprises CD21 contacting amino acid residues of C3d molecule.
XX
XX Disclosure; Page; 53pp; English.
XX
XX The invention describes a ligand of the complement receptor 2 (CD21 or
XX CD2) comprising amino acid residues 36-39 and 160-167 of the C3d
XX molecule. The ligand is useful in the manufacture of a medicament such as
XX a vaccine for modulating the immune response of a host (preferably tumour
XX vaccine), and as antigens in immunogenic compositions, therapeutics
XX diagnostic reagents, in the generation of diagnostic agents and as cancer
XX cells through the CD21/CD19 complex. Non-naturally occurring ligands and
XX site specific mutated analogues of C3d demonstrate an enhanced binding
XX affinity for CD21 as compared to the binding affinity of a wild-type C3d
XX molecule. The ligand alters the immunogenicity of an antigen, e.g. by
XX inducing or enhancing an immune response to an antigen in a host and thus
XX protects the host against disease caused by the pathogen. This sequence
XX represents the complement pathway protein C3d E37A/E39A mutant, used to
XX study the interaction of C3d with complement receptor 2 (CD21/CD2),
XX described in the method of the invention. Note: This sequence does not
XX appear in the specification but has been created from a C3d wild type
XX sequence referenced on page 11 of the invention
XX
XX Sequence 294 AA;
XX
XX Query Match 100.0%; Score 91; DB 5; Length 294;
XX Best Local Similarity 100.0%; Pred. NO. 1.2e-05;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKQLYNVEA 16
DB 224 KNRWEDPGKQLYNVEA 239
|||||
|||||

RESULT 14
AAU74859
ID AAU74859 standard; protein; 294 AA.
XX
XX AAU74859;
XX
XX 09-APR-2002 (first entry)
XX Complement pathway protein C3d, R49M mutant.
XX
XX Complement; receptor; CD21; CD2; C3d; immune response; B cell stimulator;
XX vaccine; CD21/CD19 complex; tumour; cancer; mutant; mutein.
XX
XX Homo sapiens.
XX Synthetic.

```

```

XX
XX Key Location/Qualifiers
XX Misc-difference 49
XX /note= "Wild type Arg substituted by Met"
XX
XX WO200192295-A2.
XX
XX 06-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-CA000785.
XX
XX 30-MAY-2000; 2000US-0207434P.
XX
XX (UTOR ) UNIV TORONTO.
XX
XX Isenman DE, Clemenza L;
XX WPI; 2002-114323/15.
XX
XX Ligand useful for modulating immune response such as in the preparation
XX of vaccine comprises CD21 contacting amino acid residues of C3d molecule.
XX
XX Disclosure; Page; 53pp; English.
XX
XX The invention describes a ligand of the complement receptor 2 (CD21 or
XX CD2) comprising amino acid residues 36-39 and 160-167 of the C3d
XX molecule. The ligand is useful in the manufacture of a medicament such as
XX a vaccine for modulating the immune response of a host (preferably tumour
XX vaccine), and as antigens in immunogenic compositions, therapeutics
XX diagnostic reagents, in the generation of diagnostic agents and as cancer
XX therapeutics. The ligand has the ability to bind CD21 and stimulate B
XX cells through the CD21/CD19 complex. Non-naturally occurring ligands and
XX site specific mutated analogues of C3d demonstrate an enhanced binding
XX affinity for CD21 as compared to the binding affinity of a wild-type C3d
XX molecule. The ligand alters the immunogenicity of an antigen, e.g. by
XX inducing or enhancing an immune response to an antigen in a host and thus
XX protects the host against disease caused by the pathogen. This sequence
XX represents the complement pathway protein C3d R49M mutant, used to study
XX the interaction of C3d with complement receptor 2 (CD21/CD2), described
XX in the method of the invention. Note: This sequence does not appear in
XX the specification but has been created from a C3d wild type sequence
XX referenced on page 11 of the invention
XX
XX Sequence 294 AA;
XX
XX Query Match 100.0%; Score 91; DB 5; Length 294;
XX Best Local Similarity 100.0%; Pred. NO. 1.2e-05;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKQLYNVEA 16
DB 224 KNRWEDPGKQLYNVEA 239
|||||
|||||

RESULT 15
AAU74872
ID AAU74872 standard; protein; 294 AA.
XX
XX AAU74872;
XX
XX 09-APR-2002 (first entry)
XX Complement pathway protein C3d, E166A mutant.
XX
XX Complement; receptor; CD21; CD2; C3d; immune response; B cell stimulator;
XX vaccine; CD21/CD19 complex; tumour; cancer; mutant; mutein.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 166
XX /note= "Wild type Glu substituted by Ala"
XX
XX

```

XX WO200192295-A2.
PN
XX
PD
XX
PF 30-MAY-2001; 2001WO-CA000785.
XX
PR 30-MAY-2000; 2000US-0207434P.
XX
PA (UTOR) UNIV TORONTO.
XX
PI Isenman DE, Clemenza L;
XX
DR WPI; 2002-114323/15.
XX
PT Ligand useful for modulating immune response such as in the preparation
PT of vaccine comprises CD21 contacting amino acid residues of C3d molecule.
XX
PS Disclosure; Page; 53pp; English.
XX
CC The invention describes a ligand of the complement receptor 2 (CD21 or
CC CD2) comprising amino acid residues 36-39 and 160-167 of the C3d
CC molecule. The ligand is useful in the manufacture of a medicament such as
CC a vaccine for modulating the immune response of a host (preferably tumour
CC vaccine), and as antigens in immunogenic compositions, therapeutics
CC diagnostic reagents, in the generation of diagnostic agents and as cancer
CC therapeutics. The ligand has the ability to bind CD21 and stimulate B
CC cells through the CD21/CD19 complex. Non-naturally occurring ligands and
CC site specific mutated analogues of C3d demonstrate an enhanced binding
CC affinity for CD21 as compared to the binding affinity of a wild-type C3d
CC molecule. The ligand alters the immunogenicity of an antigen, e.g. by
CC inducing or enhancing an immune response to an antigen in a host and thus
CC protects the host against disease caused by the pathogen. This sequence
CC represents the complement pathway protein C3d E166A mutant, used to study
CC the interaction of C3d with complement receptor 2 (CD21/CD2), described
CC in the method of the invention. Note: This sequence does not appear in
CC the specification but has been created from a C3d wild type sequence
CC referenced on page 11 of the invention
XX
SQ Sequence 294 AA;

Query Match 100.0%; Score 91; DB 5; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KNRWEDPGKQLYNVEA 16
Db 224 KNRWEDPGKQLYNVEA 239
|||||

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Job time : 186 secs

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OM protein - protein search, using sw model

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Title: US-09-865-281A-1

Perfect score: 91

Sequence: 1 KNRWEDPGKQLYNVEA 16

Scoring table: BLOSUM62

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Searched: 2166443 seqs, 70528306 residues

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Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80:*

1: uniprot_sprot:*

2: uniprot_treml:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	91	100.0	1663	1	CO3 HUMAN	P01024 h complemen
2	80	87.9	1663	1	CO3 RAT	P01026 rattus norv
3	79	86.8	726	1	CO3_RABIT	P12247 oryctolagus
4	77	84.6	349	2	O46544 SHEEP	O46544 ovis aries
5	76	83.5	154	2	Q29289_PIG	Q29289 sus scrofa
6	76	83.5	310	2	Q92115_MESAU	Q92115 mesocricetu
7	73	80.2	303	2	Q693V9_BOVIN	Q693V9 bos taurus
8	73	80.2	1663	1	CO3 MOUSE	P01027 m complemen
9	73	80.2	1663	2	Q80XP1_MOUSE	Q80XP1 mus musculu
10	71	78.0	1661	2	O9GKP1_PIG	O9GKP1 sus scrofa
11	58	63.7	1686	1	CO3_CAVPO	P12387 cavia porce
12	52	57.1	1399	1	RI_ARATH	O9SAC6 arabidopsis
13	52	57.1	1540	2	Q9SGX4_ARATH	O9SGX4 arabidopsis
14	51	56.0	1188	2	Q57UI3_9TRYP	Q57UI3 trypanosoma
15	50	54.9	92	2	O9MXA7_BARIN	O9MXA7 barbus inte
16	48	52.7	922	2	Q8XIG1_CLOPE	Q8XIG1 clostridium
17	47.5	52.2	373	2	Q9F2H7_STAHA	Q9F2H7 staphylococ
18	47.5	52.2	401	2	O8DYL9_STRAS	O8DYL9 streptococc
19	47.5	52.2	401	2	Q8E475_STRAS	Q8E475 streptococc
20	47	51.6	782	2	Q4WMN5_ASFPU	Q4WMN5 aspergillus
21	46.5	51.1	462	1	TILS_ENTFA	O839b3 enterococcu
22	46	50.5	79	2	O5K4Z2_BARIN	O5K4Z2 barbus inte
23	46	50.5	79	2	O5K4Z3_BARIN	O5K4Z3 barbus inte
24	46	50.5	79	2	O5K505_BARIN	O5K505 barbus inte
25	46	50.5	79	2	O5K511_BARIN	O5K511 barbus inte
26	46	50.5	79	2	O5K516_BARIN	O5K516 barbus inte
27	46	50.5	79	2	O5K520_BARIN	O5K520 barbus inte
28	46	50.5	79	2	O5K522_BARIN	O5K522 barbus inte
29	46	50.5	79	2	O5K535_BARIN	O5K535 barbus inte
30	46	50.5	79	2	O5K540_BARIN	O5K540 barbus inte
31	46	50.5	92	2	O9MXB8_BARIN	O9MXB8 barbus inte

32 46 50.5 151 2 P91717_DUGTI
33 46 50.5 192 2 Q58RX6_9HIV1
34 46 50.5 283 2 Q4RX02_TETNG
35 46 50.5 329 2 O70XU5_BARIN
36 46 50.5 400 2 Q92270_RHIOL
37 46 50.5 467 2 Q8VUW4_STAHO
38 46 50.5 546 2 Q6AP19_DESPS
39 46 50.5 652 2 Q5CLU8_CRYHO
40 46 50.5 788 2 Q4IKE0_GIBZE
41 46 50.5 1475 1 R1_CITRE
42 45 49.5 172 2 O7ZTW3_BRARE
43 45 49.5 260 2 Q6NY31_BRARE
44 45 49.5 670 2 Q5GX45_XANOR
45 45 49.5 1684 2 Q9DDV9_ONCMY

ALIGNMENTS

RESULT 1
ID CO3_HUMAN STANDARD; PRT; 1663 AA.
AC P01024;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Complement C3 precursor [Contains: Complement C3 beta chain;
DE Complement C3 alpha chain; C3a anaphylatoxin; Complement C3b alpha'
DE chain; Complement C3c fragment; Complement C3dg fragment; Complement
DE C3g fragment; Complement C3d fragment; C3f fragment].
GN Name=C3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85140166; PubMed=2579379;
RA de Bruijn M.H.L., Fey G.H.;
RT "Human complement component C3: cDNA coding sequence and derived
RT primary structure.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:708-712(1985).
RL [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS GLY-102; PRO-314;
RP LYS-863; ASP-1224 AND THR-1367.
RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA Rajkumar N., Yi Q., Nickerson D.A.;
RT "SeattleSNPs. NHGRI HL6682 program for genomic applications, UW-
RT FHRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PROTEIN SEQUENCE OF 672-748.
RX MEDLINE=76069169; PubMed=1238393;
RA Hugli T.E.;
RT "Human anaphylatoxin (C3a) from the third component of complement.
RT Primary structure.";
RL J. Biol. Chem. 250:8293-8301(1975).
RN [4]
RP PROTEIN SEQUENCE OF 955-966, AND SUBUNITS.
RX TISSUE=Serum;
RA MEDLINE=95293954; PubMed=7539791; DOI=10.1074/jbc.270.23.13645;
RA Oxvig C., Haaning J., Kristensen L., Wagner J.M., Rubin I.,
RA Stigbrand T., Gleich G.J., Sottrup-Jensen L.;
RT "Identification of angiotensinogen and complement C3dg as novel
RT proteins binding the proform of eosinophil major basic protein in
RT human pregnancy serum and plasma.";
RL J. Biol. Chem. 270:13645-13651(1995).
RN [5]
RP PROTEIN SEQUENCE OF 988-1036.
RX MEDLINE=82174534; PubMed=6175959;
RA Thomas M.L., Janatova J., Gray W.R., Tack B.F.;
RT "Third component of human complement: localization of the internal

thiolester bond."; Proc. Natl. Acad. Sci. U.S.A. 79:1054-1058(1982). [6]
RN RL
RP
RX
RA
RT
RZ
PROTEIN SEQUENCE OF 1409-1563.
MEDLINE=98154452; PubMed=3279119;
RA Daoudaki M.E., Becherer J.D., Lambiris J.D.;
RT "A 34-amino acid peptide of the third component of complement mediates
RT properdin binding."; J. Immunol. 140:1577-1580(1988). [7]
RN RL
RP
RX
RA
RT
RZ
STRUCTURE BY NMR OF C3A.
MEDLINE=88276894; PubMed=3260670;
RA Nettesheim D.G., Edalji R.P., Mollison K.W., Greer J.,
RT Zuideweg E.R.P.;
RT "Secondary structure of complement component C3a anaphylatoxin in
RT solution as determined by NMR spectroscopy: differences between
RT crystal and solution conformations."; Proc. Natl. Acad. Sci. U.S.A. 85:5036-5040(1988). [8]
RN RL
RP
RX
RA
RT
RZ
MUTAGENESIS OF THIOESTER BOND REGION.
MEDLINE=92250565; PubMed=157777;
RA Isaac L., Isenman D.E.;
RT "Structural requirements for thioester bond formation in human
RT complement component C3. Reassessment of the role of thioester bond
RT integrity on the conformation of C3."; J. Biol. Chem. 267:10062-10069(1992). [9]
RN RL
RP
RX
RA
RT
RZ
DISULFIDE BONDS.
MEDLINE=93106233; PubMed=8416818; DOI=10.1016/0014-5793(93)81139-Q;
RA Dolmer K., Sottrup-Jensen L.;
RT "Disulfide bridges in human complement component C3b."; FEBS Lett. 315:85-90(1993). [10]
RN RL
RP
RX
RA
RT
RZ
CARBOHYDRATE-LINKAGE SITE ASN-85.
MEDLINE=22660472; PubMed=12754519; DOI=10.1038/nbt827;
RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT "Identification and quantification of N-linked glycoproteins using
RT hydrazide chemistry, stable isotope labeling and mass spectrometry."; Nat. Biotechnol. 21:660-666(2003). [11]
RN RL
RP
RX
RA
RT
RZ
X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 996-1303.
MEDLINE=98259089; PubMed=9596584; DOI=10.1126/science.280.5367.1277;
RA Nagar B., Jones R.G., Diefenbach R.J., Isenman D.E., Rini J.M.;
RT "X-ray crystal structure of C3d: a C3 fragment and ligand for
RT complement receptor 2."; Science 280:1277-1281(1998). [12]
RN RL
RP
RX
RA
RT
RZ
VARIANT C3S ASN-1216.
MEDLINE=89309808; PubMed=2473125;
RA Poznansky M.C., Clissold P.M., Lachmann P.J.;
RT "The difference between human C3F and C3S results from a single amino
RT acid change from an asparagine to an aspartate residue at position
RT 1216 on the alpha-chain of the complement component, C3."; J. Immunol. 143:1254-1258(1989). [13]
RN RL
RP
RX
RA
RT
RZ
ERRATUM, AND RETRACTION.
MEDLINE=90063087; PubMed=2584723;
RA Poznansky M.C., Clissold P.M., Lachmann P.J.;
RT J. Immunol. 143:3860-3862(1989). [14]
RN RL
RP
RX
RA
RT
RZ
VARIANTS GLY-102 AND PRO-314.
MEDLINE=91011240; PubMed=1976733; DOI=10.1084/jem.172.4.1011;
RA Botta M., Yong Fong K., So A.K., Koch K., Walport M.J.;
RT "Molecular basis of polymorphisms of human complement component C3."; J. Exp. Med. 172:1011-1017(1990). [15]
RN RL
RP
RX
RA
RT
RZ
VARIANT C3 DEFICIENCY ASN-549.
MEDLINE=95050640; PubMed=7961791;
RA Singer L., Whitehead W.T., Akama H., Katz Y., Fishelson Z.,
RT Wetsel R.A.;
RT "Inherited human complement C3 deficiency. An amino acid substitution
RT in the beta-chain (Asp549 to Asn) impairs C3 secretion."; J. Biol. Chem. 269:28494-28499(1994). [16]
RN RL
RP
RX
RA
RT
RZ
VARIANT C3 DEFICIENCY GLN-1320.
Watanabe Y., Matsui N., Yan K., Nishimukai H., Tokunaga K., Juji T.,
RA Kobayashi N., Kohsaka T.;
RT "A novel C3 allotype C3'F02' has an amino acid substitution that may
RT inhibit iC3b synthesis and cause C3-hypocomplementemia."; Mol. Immunol. 30:62-62(1993).
CC -!- FUNCTION: C3 plays a central role in the activation of the
CC complement system. Its processing by C3 convertase is the central
CC reaction in both classical and alternative complement pathways.
CC After activation C3b can bind covalently, via its reactive
CC thiolester, to cell surface carbohydrates or immune aggregates.
CC -!- FUNCTION: Derived from proteolytic degradation of complement C3,
CC C3a anaphylatoxin is a mediator of local inflammatory process. It
CC induces the contraction of smooth muscle, increases vascular
CC permeability and causes histamine release from mast cells and
CC basophilic leukocytes.
CC -!- SUBUNIT: C3 precursor is first processed by the removal of 4 Arg
CC residues, forming two chains, beta and alpha, linked by a
CC disulfide bond. C3 convertase activates C3 by cleaving the alpha
CC chain, releasing C3a anaphylatoxin and generating C3b (beta chain
CC + alpha' chain). During pregnancy, C3dg exists as a complex
CC (probably a 2:1:2 heterohexamer) with AGT and the proform of PRG2.
CC -!- PTM: C3b is rapidly split in two positions by factor I and a
CC cofactor to form iC3b (inactivated C3b) and C3f which is released.
CC Then iC3b is slowly cleaved (possibly by factor I) to form C3c and
CC C3dg. Other proteases produce other fragments such as C3d or C3g.
CC -!- POLYMORPHISM: There are two alleles: C3S (C3 slow), the most
CC common allele in all races and C3F (C3 fast), relatively frequent
CC in Caucasoids, less common in Black Americans, extremely rare in
CC Orientals.
CC -!- DISEASE: Defects in C3 are the cause of C3 deficiency
CC [MIM:120700]. It can result in susceptibility to pyogenic
CC infection.
CC -!- SIMILARITY: Contains 1 anaphylatoxin-like domain.
CC -!- SIMILARITY: Contains 1 NTR domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; K02765; AA85332.1; -; mRNA.
CC EMBL; AF513239; AAR89906.1; -; Genomic_DNA.
CC PIR; A94065; C3HU.
CC PDB; 1C3D; X-ray; @=-.
CC PDB; 1GHQ; X-ray; A=996-1300.
CC GlycoSuiteDB; P01024; -.
CC SWISS-2DPAGE; P01024; HUMAN.
CC Sienna-2DPAGE; P01024; -.
CC Ensemble; ENSG00000125730; Homo sapiens.
CC HGNC; HGNC:1318; C3.
CC MIM; 120700; -.
CC GO; GO:0005102; F:receptor binding; TAS.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
CC GO; GO:0006955; P:immune response; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR011626; A2M_comp.
CC InterPro; IPR002890; A2M_N.
CC InterPro; IPR011625; A2M_N2.
CC InterPro; IPR011627; A2M_receptor.
CC InterPro; IPR000020; Anaphylatoxin.
CC InterPro; IPR001840; Anaphylatoxn.
CC InterPro; IPR001599; MacrogloblnA2.
CC InterPro; IPR001134; Netrin_C.
CC Pfam; PF00207; A2M; 1.
CC Pfam; PF07678; A2M_comp; 1.
CC Pfam; PF01835; A2M_N; 1.
CC Pfam; PF07703; A2M_N2; 1.
CC Pfam; PF07677; A2M_recep; 1.
CC Pfam; PF01821; ANATO; 1.
CC Pfam; PF01759; NTR; 1.

DR PRINTS; PR00004; ANAPHYLATOXN.
 DR ProDom; PD003264; Anaphylatoxin; 1.

Query Match 100.0%; Score 91; DB 1; Length 1663;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWDPGKQLYNVEA 16
 |||||
 Db 1217 KNRWDPGKQLYNVEA 1332

RESULT 2
 CO3 RAT STANDARD; PRT; 1663 AA.

AC P01026;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Complement C3 precursor [Contains: Complement C3 beta chain;
 DE Complement C3 alpha chain; C3a anaphylatoxin; Complement C3b alpha'
 DE chain].
 GN Name=C3;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Liver;
 RX MEDLINE=90245672; PubMed=2336397;
 RA Miumi Y., Sohma M., Ikehara Y.;
 RT "Nucleotide and deduced amino acid sequence of rat complement C3.";
 RL Nucleic Acids Res. 18:2178-2178(1990).
 RN [2]
 RP PROTEIN SEQUENCE OF 671-748.
 RX MEDLINE=79062262; PubMed=309768;
 RA Jacobs J.W., Rubin J.S., Hugli T.E., Bogardt R.A. Jr., Mariz I.K.,
 Daniels J.S., Daughaday W.H., Bradshaw R.A.;
 RT "Purification, characterization, and amino acid sequence of rat
 anaphylatoxin (C3a).";
 RL Biochemistry 17:5031-5038(1978).
 RN [3]
 RP NUCLEOTIDE SEQUENCE OF 1316-1595.
 RX MEDLINE=89380332; PubMed=2674144;
 RA Sundstrom S.A., Komm B.S., Ponce-De-Leon H., Yi Z., Teuscher C.,
 Lyttle C.R.;
 RT "Estrogen regulation of tissue-specific expression of complement C3.";
 RL J. Biol. Chem. 264:16941-16947(1989).
 CC -1- FUNCTION: C3 plays a central role in the activation of the
 complement system. Its processing by C3 convertase is the central
 reaction in both classical and alternative complement pathways.
 After activation C3b can bind covalently, via its reactive
 thioester, to cell surface carbohydrates or immune aggregates.
 CC -1- FUNCTION: Derived from proteolytic degradation of complement C3,
 C3a anaphylatoxin is a mediator of local inflammatory process. It
 induces the contraction of smooth muscle, increases vascular
 permeability and causes histamine release from mast cells and
 basophilic leukocytes.
 CC -1- SUBUNIT: C3 precursor is first processed by the removal of 4 Arg
 residues, forming two chains, beta and alpha, linked by a
 disulfide bond. C3 convertase activates C3 by cleaving the alpha
 chain, releasing C3a anaphylatoxin and generating C3b (beta chain
 + alpha' chain).
 CC -1- SIMILARITY: Contains 1 anaphylatoxin-like domain.
 CC -1- SIMILARITY: Contains 1 NTR domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC -----
 DR EMBL; X52477; CAA36716.1; -; mRNA.
 DR EMBL; M29866; AAA40837.1; ALT_SEQ; mRNA.
 DR PIR; S15764; C3RT.
 DR PDB; 1QOF; X-ray; A=1010-1286.
 DR PDB; 1Q5J; X-ray; A/B/C/D=1010-1286.
 DR RGD; 2232; C3.
 DR InterPro; IPR011626; A2M comp.
 DR InterPro; IPR002890; A2M_N.
 DR InterPro; IPR011625; A2M_N_2.
 DR InterPro; IPR011627; A2M_receptor.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR001840; Anaphylatoxin.
 DR InterPro; IPR001599; MacroglobulinA2.
 DR InterPro; IPR001134; Netrin_C.
 DR Pfam; PF00207; A2M; 1.
 DR Pfam; PF07678; A2M comp; 1.
 DR Pfam; PF01835; A2M_N; 1.
 DR Pfam; PF07703; A2M_N_2; 1.
 DR Pfam; PF07677; A2M_recep; 1.
 DR Pfam; PF01821; ANATO; 1.
 DR Pfam; PF01759; NTR; 1.
 DR PRINTS; PR00004; ANAPHYLATOXN.
 DR ProDom; PD003264; Anaphylatoxin; 1.
 DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
 DR PROSITE; PS50189; NTR; 1.
 DR 3D-structure; Complement alternate pathway; Complement pathway;
 KW Direct protein sequencing; Glycoprotein; Immune response;
 KW Inflammatory response; Innate immunity; Plasma; Signal;
 KW Thioester bond.
 FT SIGNAL 1 24
 FT CHAIN 25 1663
 FT CHAIN 25 666
 FT CHAIN 671 1663
 FT PEPTIDE 671 748
 FT CHAIN 749 1663
 FT DOMAIN 693 728
 FT DOMAIN 1518 1661
 FT SITE 748 749
 FT CARBOHYD 939 939
 FT CARBOHYD 1617 1617
 FT DISULFID 558 816
 FT DISULFID 626 661
 FT DISULFID 693 720
 FT DISULFID 694 727
 FT DISULFID 707 728
 FT DISULFID 873 1513
 FT DISULFID 1101 1158
 FT DISULFID 1358 1489
 FT DISULFID 1389 1458
 FT DISULFID 1506 1511
 FT DISULFID 1518 1590
 FT DISULFID 1537 1661
 FT CROSSLNK 1010 1013
 FT CONFLICT 721 722
 FT TURN 1011 1012
 FT HELIX 1013 1031
 FT TURN 1032 1032
 FT HELIX 1034 1037
 FT HELIX 1039 1041
 FT HELIX 1042 1057
 FT TURN 1058 1059
 FT STRAND 1060 1060
 FT TURN 1062 1063
 FT STRAND 1066 1066
 FT TURN 1070 1071
 FT HELIX 1076 1089
 FT TURN 1090 1092
 FT HELIX 1097 1111
 FT STRAND 1112 1112
 Complement C3.
 Complement C3 beta chain.
 Complement C3 alpha chain.
 C3a anaphylatoxin.
 Complement C3b alpha' chain.
 Anaphylatoxin-like.
 NTR.
 Cleavage (by C3 convertase).
 N-linked (GlcNAc...) (Probable).
 N-linked (GlcNAc...) (Probable).
 Interchain (between beta and alpha
 chains) (By similarity).
 By similarity.
 By similarity.
 By similarity.
 By similarity.
 By similarity.
 By similarity.
 By similarity.
 By similarity.
 By similarity.
 Isoglutamyl cysteine thioester (Cys-Gln).
 LK -> KL (in Ref. 2).

```

FT TURN      1114      1115
FT STRAND    1118      1118
FT HELIX     1127      1134
FT TURN      1137      1138
FT HELIX     1139      1158
FT TURN      1159      1161
FT TURN      1163      1164
FT HELIX     1165      1180
FT TURN      1181      1182
FT HELIX     1186      1198
FT TURN      1199      1200
FT TURN      1204      1205
FT HELIX     1206      1213
FT STRAND    1215      1215
FT TURN      1216      1218
FT STRAND    1219      1219
FT TURN      1223      1224
FT HELIX     1226      1242
FT TURN      1243      1244
FT TURN      1246      1247
FT HELIX     1249      1258
FT TURN      1263      1264
FT TURN      1266      1267
FT HELIX     1269      1285
SQ SEQUENCE  1663 AA; 186460 MW; 2F87CCB143CDD4BC CRC64;

Query Match      87.9%; Score 80; DB 1; Length 1663;
Best Local Similarity 81.2%; Pred. No. 0.00023;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNRWEDPGKQLYNVEA 16
DB      1217 RNRWEEPGQQLYNVEA 1232

RESULT 3
CO3_RABIT
ID_CO3_RABIT STANDARD; PRT; 726 AA.
AC P12247;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Complement C3 alpha chain (Fragment).
GN Name=C3;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=8706907; PubMed=3019881;
RA Kusano M., Choi N.H., Tomita M., Yamamoto K., Migita S., Sekiya T.,
RA Nishimura S.;
RT "Nucleotide sequence of cDNA and derived amino acid sequence of rabbit
RT complement component C3 alpha-chain."
RL Immunol. Invest. 15:365-378(1986).
CC -1- FUNCTION: C3 plays a central role in the activation of the
CC complement system. Its processing by C3 convertase is the central
CC reaction in both classical and alternative complement pathways.
CC After activation C3b can bind covalently, via its reactive
CC thioester, to cell surface carbohydrates or immune aggregates.
CC -1- SUBUNIT: C3 precursor is first processed by the removal of 4 Arg
CC residues, forming two chains, beta and alpha, linked by a
CC disulfide bond. C3 convertase activates C3 by cleaving the alpha
CC chain, releasing C3a anaphylatoxin and generating C3b (beta chain
CC + alpha' chain).
CC -1- SIMILARITY: Contains 1 NTR domain.
CC -----
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CC use as long as its content is in no way modified and this statement is not

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CC removed.
CC -----
DR EMBL; M32434; AA31190.1; -; mRNA.
DR FIR; A27602; A27602.
DR HSSP; P01024; 1C3D.
DR SMR; P12247; 58-362.
DR InterPro; IPR011626; A2M comp.
DR InterPro; IPR011627; A2M_receptor.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR001599; MacrogloblnA2.
DR InterPro; IPR001134; Netrin_C.
DR Pfam; PF07678; A2M_comp; 1.
DR Pfam; PF07677; A2M_recep; 1.
DR Pfam; PF01759; NTR; 1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; PARTIAL.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; PARTIAL.
DR PROSITE; PS0189; NTR; 1.
DR Complement alternate pathway; Complement pathway; Glycoprotein;
KW Immune response; Inflammatory response; Innate immunity; Plasma;
KW Thioester bond.
FT CHAIN <1 726 Complement C3 alpha chain.
FT DOMAIN 581 724 NTR.
FT CARBOHYD 2 2 N-linked (GlcNAc..)(Potential).
FT CARBOHYD 233 233 N-linked (GlcNAc..)(Potential).
FT CARBOHYD 680 680 N-linked (GlcNAc..)(Potential).
FT CROSSLINK 73 76 isoglutamyl cysteine thioester (Cys-Gln).
FT NON_TER 1 1
SQ SEQUENCE 726 AA; 81844 MW; F4B4C35D461300E9 CRC64;

Query Match      86.8%; Score 79; DB 1; Length 726;
Best Local Similarity 81.2%; Pred. No. 0.00013;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNRWEDPGKQLYNVEA 16
DB      280 KNRWEEPGQQLYNVEA 295

RESULT 4
O46544 SHEEP
ID O46544 SHEEP PRELIMINARY; PRT; 349 AA.
AC O46544;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Complement component C3 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=white alpine; TISSUE=Liver;
RX MEDLINE=9830947; PubMed=9647256;
RA Hein W.R., Dudler L., Marston W.L., Landeverk T., Young A.J.,
RA Avila D.;
RT "Ubiquitination and dimerization of complement receptor type 2 on
RT sheep B cells."
RL J. Immunol. 161:458-466(1998).
DR EMBL; AF038130; AAB92374.2; -; mRNA.
DR HSSP; P01026; 1QGF.
DR SMR; O46544; 19-322.
DR GO; GO:0004866; F:endoropeptidase inhibitor activity; IEA.
DR InterPro; IPR011626; A2M_comp.
DR InterPro; IPR001599; MacrogloblnA2.
DR Pfam; PF07678; A2M_comp; 1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR NON_TER 1 1
FT NON_TER 349 349
SQ SEQUENCE 349 AA; 39679 MW; 70C2023E42ED5EE3 CRC64;

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Query Match      84.6%; Score 77; DB 2; Length 349;
Best Local Similarity 81.2%; Pred. No. 0.00013;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNRWEDPGKOLYNVEA 16
Db 241 KNRWEPNKKLYNVEA 256

RESULT 5
Q29289_PIG PRELIMINARY; PRT; 154 AA.
AC Q29289;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Complement C3 (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Small intestine;
RX MEDLINE=96327607; PubMed=8672129; DOI=10.1007/s003359900153;
RA Winteroe A.K., Fredholm M., Davies W.;
RT "Evaluation and characterization of a porcine small intestine cDNA
RT library: analysis of 839 clones.";
RL Mamm. Genome 7:509-517(1996).
DR EMBL; F1640; CAA23173.1; -; mRNA.
DR HSSP; P01026; 1QQF.
DR SMR; Q29289; 8-91.
DR InterPro; IPR011626; A2M_comp.
DR Pfam; PF07678; A2M_comp; 1.
FT NON_TER 1 154
FT NON_TER 154 154
SQ SEQUENCE 154 AA; 17440 MW; 6DC7661C1253ED45 CRC64;

Query Match      83.5%; Score 76; DB 2; Length 154;
Best Local Similarity 75.0%; Pred. No. 7.8e-05;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKOLYNVEA 16
Db 10 KNRWEPGKOLYNVEA 25

RESULT 6
Q92115_MESAU PRELIMINARY; PRT; 310 AA.
AC Q92115;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Complement C3 (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetinae; Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yamamoto K., Inoue N., Sakiyama H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB024425; BAA75923.1; -; mRNA.
DR HSSP; P01026; 1QQF.
DR SMR; Q92115; 18-293.
DR GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.
DR InterPro; IPR011626; A2M_comp.
DR InterPro; IPR001599; MacroglublnA2.
DR Pfam; PF07678; A2M_comp; 1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
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FT NON_TER 1 1
FT NON_TER 310 310
SQ SEQUENCE 310 AA; 34779 MW; 11ED3BEEF82D327D CRC64;

Query Match      83.5%; Score 76; DB 2; Length 310;
Best Local Similarity 75.0%; Pred. No. 0.00017;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKOLYNVEA 16
Db 224 KNRWEPGKOLYNVEA 239

RESULT 7
Q693V9_BOVIN PRELIMINARY; PRT; 303 AA.
ID Q693V9_BOVIN PRELIMINARY; PRT; 303 AA.
AC Q693V9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Complement component C3d (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hodgins D., Firth M., Pei Y., Yoo D., Shewen P.;
RT "Cloning, Sequencing and Analysis of the C3d Fragment of Bovine
RT Complement Component 3.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV630404; AAT76518.1; -; mRNA.
DR SMR; Q693V9; 1-298.
DR GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.
DR InterPro; IPR011626; A2M_comp.
DR InterPro; IPR001599; MacroglublnA2.
DR Pfam; PF07678; A2M_comp; 1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
FT NON_TER 1 1
FT NON_TER 303 303
SQ SEQUENCE 303 AA; 34443 MW; 2F3A15020CEA3797 CRC64;

Query Match      80.2%; Score 73; DB 2; Length 303;
Best Local Similarity 75.0%; Pred. No. 0.00056;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNRWEDPGKOLYNVEA 16
Db 216 KNRWEPNKKLYNVEA 231

RESULT 8
CO3_MOUSE PRELIMINARY; PRT; 1663 AA.
ID CO3_MOUSE STANDARD; PRT; 1663 AA.
AC P01027; Q61370;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Complement C3 precursor (HSE-MSF) [Contains: Complement C3 beta chain;
DE Complement C3 alpha chain; C3a anaphylatoxin; Complement C3b alpha
DE chain; Complement C3c fragment; Complement C3dg fragment; Complement
DE C3g fragment; Complement C3d fragment; Complement C3, isoform Short;
DE C3f fragment].
GN Name=C3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM LONG).
RX MEDLINE=85038854; PubMed=6208565;
```

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RA Fey G.H., Lundwall A., Wetsel R.A., Tack B.F., de Bruijn M.H.L.,
RA Domdey H.;
RA "Nucleotide sequence of complementary DNA and derived amino acid
RT sequence of murine complement protein C3.";
RT Philos. Trans. R. Soc. Lond., B, Biol. Sci. 306:333-344(1984).
RL [2]
RN
RP NUCLEOTIDE SEQUENCE OF 1-724 (ISOFORM LONG).
RX MEDLINE=85054818; PubMed=6548745;
RA Lundwall A., Wetsel R.A., Domdey H., Tack B.F., Fey G.H.;
RA "Structure of murine complement component C3. I. Nucleotide sequence
RT of cloned complementary and genomic DNA coding for the beta chain.";
RL J. Biol. Chem. 259:13851-13856(1984).
RN [3]
RN NUCLEOTIDE SEQUENCE OF 25-1663 (ISOFORM LONG).
RX MEDLINE=85113177; PubMed=2578664;
RA Sottrup-Jensen L., Stepanik T.M., Kristensen T., Lonblad P.B.,
RA Jones C.M., Wierzbicki D.M., Magnusson S., Domdey H., Wetsel R.A.,
RA Lundwall A., Tack B.F., Fey G.H.;
RA "Common evolutionary origin of alpha 2-macroglobulin and complement
RT components C3 and C4.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:9-13(1985).
RN [4]
RN NUCLEOTIDE SEQUENCE OF 25-240 (ISOFORM LONG).
RX MEDLINE=84045280; PubMed=6356427; DOI=10.1007/BF00205869;
RA Fey G., Domdey H., Wiebauer K., Whitehead A.S., Odink K.;
RA "Structure and expression of the C3 gene.";
RL Springer Semin. Immunopathol. 6:119-147(1983).
RN [5]
RN NUCLEOTIDE SEQUENCE OF 671-1663 (ISOFORM LONG).
RX MEDLINE=85054819; PubMed=6094532;
RA Wetsel R.A., Lundwall A., Davidson F., Gibson T., Tack B.F., Fey G.H.;
RA "Structure of murine complement component C3. II. Nucleotide sequence
RT of cloned complementary DNA coding for the alpha chain.";
RL J. Biol. Chem. 259:13857-13862(1984).
RN [6]
RN NUCLEOTIDE SEQUENCE OF 671-748.
RX MEDLINE=83117730; PubMed=6961437;
RA Domdey H., Wiebauer K., Kazmaier M., Mueller V., Odink K., Fey G.H.;
RA "Characterization of the mRNA and cloned cDNA specifying the third
RT component of mouse complement.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:7619-7623(1982).
RN [7]
RN NUCLEOTIDE SEQUENCE OF 658-761.
RX MEDLINE=84201365; PubMed=6603661;
RA Fey G.H., Wiebauer K., Domdey H.;
RA "Amino acid sequences of mouse complement C3 derived from nucleotide
RT sequences of cloned cDNA.";
RL Ann. N. Y. Acad. Sci. 421:307-312(1983).
RN [8]
RN NUCLEOTIDE SEQUENCE OF 1-34.
RX MEDLINE=83117622; PubMed=6985486;
RA Wiebauer K., Domdey H., Diggelmann H., Fey G.;
RA "Isolation and analysis of genomic DNA clones encoding the third
RT component of mouse complement.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:7077-7081(1982).
RN [9]
RN PROTEIN SEQUENCE OF 25-41 AND 749-760.
RX MEDLINE=93373334; PubMed=8364938;
RA Hamada J.-I., Cavanaugh P.G., Miki K., Nicolson G.L.;
RA "A paracrine migration-stimulating factor for metastatic tumor cells
RT secreted by mouse hepatic sinusoidal endothelial cells: identification
RT as complement component C3b.";
RL Cancer Res. 53:4418-4423(1993).
RN [10]
RN PROTEIN SEQUENCE OF 25-31 AND 671-680.
RX MEDLINE=91293304; PubMed=2065778; DOI=10.1016/0014-5793(91)80715-F;
RA Sato T., Hong M.H., Jin C.H., Ishimi Y., Udagawa N., Shinki T.,
RA Abe E., Suda T.;
RA "The specific production of the third component of complement by
RT osteoblastic cells treated with 1 alpha,25-dihydroxyvitamin D3.";
RL FEBS Lett. 285:21-24(1991).
RN [11]
RN ALTERNATIVE INITIATION.
RX MEDLINE=95053742; PubMed=7964485; DOI=10.1084/jem.180.6.2079;
RA Cahen-Kramer Y., Martenson I.B., Melchers F.;
RA "The structure of an alternate form of complement C3 that displays
RT costimulatory growth factor activity for B lymphocytes.";
RL J. Exp. Med. 180:2079-2088(1994).
RN [-] FUNCTION: C3 plays a central role in the activation of the
CC complement system. Its processing by C3 convertase is the central
CC reaction in both classical and alternative complement pathways.
CC After activation C3b can bind covalently, via its reactive
CC thiolester, to cell surface carbohydrates or immune aggregates.
CC [-] FUNCTION: Derived from proteolytic degradation of complement C3,
CC C3a anaphylatoxin is a mediator of local inflammatory process. It
CC induces the contraction of smooth muscle, increases vascular
CC permeability and causes histamine release from mast cells and
CC basophilic leukocytes. The short isoform has B-cell stimulatory
CC activity.
CC [-] SUBUNIT: C3 precursor is first processed by the removal of 4 Arg
CC residues, forming two chains, beta and alpha, linked by a
CC disulfide bond. C3 convertase activates C3 by cleaving the alpha
CC chain, releasing C3a anaphylatoxin and generating C3b (beta chain
CC + alpha' chain).
CC [-] ALTERNATIVE PRODUCTS:
CC Event=Alternative initiation;
CC Comment=2 isoforms, Long (shown here) and Short, are produced by
CC alternative initiation;
CC Conector to form iC3b (inactivated C3b) and C3f which is released.
CC Then iC3b is slowly cleaved (possibly by factor I) to form C3c and
CC C3dg. Other proteases produce other fragments such as C3d or C3g.
CC [-] SIMILARITY: Contains 1 anaphylatoxin-like domain.
CC [-] SIMILARITY: Contains 1 NTR domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL: K02782; AAC42013.1; -; mRNA.
CC EMBL: J00369; AAA37336.1; -; Genomic DNA.
CC EMBL: J00367; AAA37336.1; JOINED; Genomic DNA.
CC EMBL: M35659; AAA37339.1; -; mRNA.
CC EMBL: M33032; AAA37378.1; -; mRNA.
CC EMBL: Z37998; CAA86099.2; -; Genomic DNA.
CC FIR: A92459; C3MS.
CC HSP: P01026; IQQF.
CC SMR: P01027; 1011-1286.
CC Ensembl: ENSMUSG00000024164; Mus musculus.
CC MGI: MGI:88227; C3.
CC GO: GO:0005615; C:extracellular space; TAS.
CC GO: GO:0005515; F:protein binding; IPI.
CC GO: GO:0050766; P:positive regulation of phagocytosis; IMP.
CC GO: GO:0001798; P:positive regulation of type Iia hypersensit. .; IMP.
CC InterPro: IPR011626; A2M comp.
CC InterPro: IPR002890; A2M_N.
CC InterPro: IPR011625; A2M_N_2.
CC InterPro: IPR011627; A2M_receptor.
CC InterPro: IPR000020; Anaphylatoxin.
CC InterPro: IPR001840; Anaphylatoxn.
CC InterPro: IPR001599; MacroglobinA2.
CC InterPro: IPR001134; Netrin_C.
CC Pfam: PF00207; A2M; 1.
CC Pfam: PF07678; A2M_comp; 1.
CC Pfam: PF01835; A2M_N; 1.
CC Pfam: PF07703; A2M_N_2; 1.
CC Pfam: PF07677; A2M_recep; 1.
CC Pfam: PF01821; ANATO; 1.
CC Pfam: PF01759; NTR; 1.
CC PRINTS: PR00004; ANAPHYLATOXN.
CC PRODOM: PD003284; Anaphylatoxin; 1.
CC PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.
CC PROSITE: PS01177; ANAPHYLATOXIN_1; 1.
CC PROSITE: PS01178; ANAPHYLATOXIN_2; 1.

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DR PROSITE; PS50189; NTR; 1.
 KW Alternative initiation; Complement alternate pathway;
 KW Complement pathway; Direct protein sequencing; Glycoprotein;
 KW Immune response; Inflammatory response; Innate immunity; Plasma;
 KW Signal; Thioester bond.

FT SIGNAL 1 24
 FT CHAIN 25 1663 Complement C3, isoform Long.
 FT CHAIN 25 666 Complement C3 beta chain.
 FT CHAIN 671 1663 Complement C3 alpha chain.
 FT CHAIN 671 748 C3a anaphylatoxin.
 FT CHAIN 749 1663 Complement C3b alpha' chain.
 FT CHAIN 749 954 Complement C3c fragment.
 FT CHAIN 955 1303 Complement C3dg fragment.
 FT CHAIN 955 1001 Complement C3g fragment.
 FT CHAIN 1002 1303 Complement C3d fragment.
 FT CHAIN 1129 1663 Complement C3, isoform Short.
 FT INIT_MET 1129 1129 For isoform Short.
 FT PEPTIDE 1304 1320 C3f fragment.
 FT DOMAIN 693 728 Anaphylatoxin-like.
 FT SITE 1518 1661 NTR.
 FT SITE 748 749 Cleavage (by C3 convertase).
 FT SITE 1303 1304 Cleavage (by factor I).
 FT SITE 1320 1321 Cleavage (by factor I).
 FT CARBOHYD 939 939 N-linked (GlcNAc...).
 FT CARBOHYD 1617 1617 N-linked (GlcNAc...).
 FT DISULFID 559 816 Interchain (between beta and alpha chains) (By similarity).
 FT DISULFID 626 661 By similarity.
 FT DISULFID 693 720 By similarity.
 FT DISULFID 694 727 By similarity.
 FT DISULFID 707 728 By similarity.
 FT DISULFID 873 1513 By similarity.
 FT DISULFID 1101 1158 By similarity.
 FT DISULFID 1358 1458 By similarity.
 FT DISULFID 1389 1489 By similarity.

Query Match 80.2%; Score 73; DB 1; Length 1663;
 Best Local Similarity 75.0%; Pred. No. 0.0038;
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNRWDPGKQLYNVEA 16
 :|||:|:|||||
 DB 1217 RNRWEPDQQLYNVEA 1232

RESULT 9
 Q80XPI_MOUSE
 ID Q80XPI_MOUSE PRELIMINARY; PRT; 1663 AA.
 AC Q80XPI;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Complement component 3.
 GN Name=C3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=FVB/N; TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uudin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., D.E.,
 RA Butterfield Y.S.N., Krzywinski M.L., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC043338; AA43338.1; -, mRNA.
 DR HSSP; P01026; 1QQF.
 DR SMR; Q80XPI; 1011-1286.
 DR MGI; MGI:88227; C3.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005515; P:protein binding; IPI.
 DR GO; GO:0050766; P:positive regulation of phagocytosis; IMP.
 DR GO; GO:0001799; P:positive regulation of type IIa hypersensit. .; IMP.
 DR InterPro; IPR011626; A2M_comp.
 DR InterPro; IPR002890; A2M_N.
 DR InterPro; IPR011625; A2M_N.2.
 DR InterPro; IPR011627; A2M_receptor.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR001840; Anaphylatoxin.
 DR InterPro; IPR001599; MacroglobinA2.
 DR InterPro; IPR001134; Netrin_C.
 DR Pfam; PF00207; A2M; 1.
 DR Pfam; PF07678; A2M_comp; 1.
 DR Pfam; PF01835; A2M_N; 1.
 DR Pfam; PF07703; A2M_N.2; 1.
 DR Pfam; PF07677; A2M_recep; 1.
 DR Pfam; PF01821; ANATO; 1.
 DR Pfam; PF01759; NTR; 1.
 DR PRINTS; PR00004; ANAPHYLATOXN.
 DR ProDom; PD003264; Anaphylatoxin; 1.
 DR SMART; SM00104; ANATO; 1.
 DR SMART; SM00643; C345C; 1.
 DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
 DR PROSITE; PS01177; ANAPHYLATOXIN 1; 1.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
 DR PROSITE; PS50189; NTR; 1.
 SQ SEQUENCE 1663 AA; 186483 MW; 7E5546CC7C314779 CRC64;
 Query Match 80.2%; Score 73; DB 2; Length 1663;
 Best Local Similarity 75.0%; Pred. No. 0.0038;
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KNRWDPGKQLYNVEA 16
 :|||:|:|||||
 DB 1217 RNRWEPDQQLYNVEA 1232

RESULT 10

Q80XPI_MOUSE

ID Q80XPI_MOUSE PRELIMINARY; PRT; 1661 AA.

AC Q80XPI;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DE Complement component C3 (Complement C3).

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;

OC Sus.

OC NCBI_TaxID=9823;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Liver;

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RX MEDLINE=21313047; PubMed=11419349;
RA Wimmers K., Mekchay S., Ponsuksilli S., Hardge T., Yerle M.,
RA Schellander K.;
RT "Polymorphic sites in exon 15 and 30 of the porcine C3 gene.";
RN Anim. Genet. 32:46-47(2001).
RN [2].
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Liver;
RC TISSUE=Liver;
RA Wimmers K., Ponsuksilli S., Schmall F., Schellander K.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [3].
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Liver;
RC TISSUE=Liver;
RX MEDLINE=22444329; PubMed=12557038;
RA Wimmers K., Mekchay S., Schellander K., Ponsuksilli S.;
RT "Molecular characterization of the pig C3 gene and its association
RT with complement activity.";
RL Immunogenetics 54:714-724(2003).
RN [4].
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Liver;
RC TISSUE=Liver;
RA Wimmers K., Mekchay S., Schellander K., Ponsuksilli S.;
RT "Molecular characterization of the pig C3 gene and its association
RT with complement activity.";
RL Immunogenetics 54:714-724(2003).
DR EMBL; AF154933; AA040365.1; -; mRNA.
DR EMBL; AJ494748; CAD38823.2; -; Genomic_DNA.
DR HSSP; P01026; 1QQF.
DR SMR; Q9GKPL; 993-1297.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.
DR GO; GO:0006958; P:complement activation, classical pathway; IEA.
DR GO; GO:0006954; P:inflammatory response; IEA.
DR InterPro; IPR011626; A2M_comp.
DR InterPro; IPR002890; A2M_N.
DR InterPro; IPR011625; A2M_N_2.
DR InterPro; IPR011627; A2M_Receptor.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR001840; Anaphylatoxn.
DR InterPro; IPR001599; MacrogloblnA2.
DR InterPro; IPR001134; Netrin_C.
DR Pfam; PF00207; A2M; 1.
DR Pfam; PF07678; A2M_comp; 1.
DR Pfam; PF01835; A2M_N; 1.
DR Pfam; PF07703; A2M_N_2; 1.
DR Pfam; PF07677; A2M_recep; 1.
DR Pfam; PF01821; ANATO; 1.
DR Pfam; PF01759; NTR; 1.
DR PRINTS; PR00004; ANAPHYLATOXN.
DR ProDom; PD003264; Anaphylatoxin; 1.
DR SMART; SM00104; ANATO; 1.
DR SMART; SM00643; C345C; 1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 1661 AA; 186805 MW; 4899D0914BE3310C CRC64;

Query Match 78.0%; Score 71; DB 2; Length 1661;
Best Local Similarity 68.8%; Pred. No. 0.0084;
Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVEA 16
:|||||:|||||:
Db 1215 RNRWEPGQKLHNVEA 1230

RESULT 11
CO3_CAVPO
ID -CO3_CAVPO STANDARD; PRT; 1666 AA.
AC P12387;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)

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DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Complement C3 precursor [Contains: Complement C3 beta chain;
DE Complement C3 alpha chain; C3a anaphylatoxin; Complement C3b alpha'
DE chain; Complement C3d fragment].
GN Name=C3;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1].
RN NUCLEOTIDE SEQUENCE [mRNA].
RP STRAIN=Hartley; TISSUE=Liver;
RX MEDLINE=90307998; PubMed=19731176;
RA Auerbach H.S., Burger R., Dodds A., Colten H.R.;
RT "Molecular basis of complement C3 deficiency in guinea pigs.";
RL J. Clin. Invest. 86:96-106(1990).
RN [2].
RN PROTEIN SEQUENCE OF 23-38.
RP TISSUE=Macrophage;
RX MEDLINE=82075767; PubMed=6458605;
RA Goldberger G., Thomas M.L., Tack B.F., Williams J., Colten H.R.,
RA Abraham G.N.;
RT "NH2-terminal structure and cleavage of guinea pig pro-C3, the
RT precursor of the third complement component.";
RL J. Biol. Chem. 256:12617-12619(1981).
RN [3].
RN PROTEIN SEQUENCE OF 23-38; 676-687 AND 993-1032, AND THIOESTER BOND.
RX TISSUE=Plasma;
RX MEDLINE=83178889; PubMed=6838833;
RA Thomas M.L., Tack B.F.;
RT "Identification and alignment of a thiol ester site in the third
RT component of guinea pig complement.";
RL Biochemistry 22:942-947(1983).
RN [4].
RN PROTEIN SEQUENCE OF 676-753.
RX MEDLINE=89113342; PubMed=3064079;
RA Gerard N.P., Lively M.O., Gerard C.;
RT "Amino acid sequence of guinea pig C3a anaphylatoxin.";
RN Protein Seq. Data Anal. 1:473-478(1988).
CC -!- FUNCTION: C3 plays a central role in the activation of the
CC complement system. Its processing by C3 convertase is the central
CC reaction in both classical and alternative complement pathways.
CC After activation C3b can bind covalently, via its reactive
CC thioester, to cell surface carbohydrates or immune aggregates.
CC -!- FUNCTION: Derived from proteolytic degradation of complement C3,
CC C3a anaphylatoxin is a mediator of local inflammatory process. It
CC induces the contraction of smooth muscle, increases vascular
CC permeability and causes histamine release from mast cells and
CC basophilic leukocytes.
CC -!- PTM: First processed by the removal of 4 Arg residues by furin-
CC type protease, forming two chains, alpha and gamma/beta precursor,
CC linked by a disulfide bond. C3 convertase activates C3 by cleaving
CC the alpha chain, releasing C3a anaphylatoxin and generating C3b
CC (beta chain + alpha' chain). Processing by elastase produces the
CC C3d fragment.
CC -!- SIMILARITY: Contains 1 anaphylatoxin-like domain.
CC -!- SIMILARITY: Contains 1 NTR domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M34054; AAA37038.1; -; mRNA.
DR PIR; A37156; C3GP.
DR HSSP; P01026; 1QQF.
DR InterPro; IPR011626; A2M_comp.
DR InterPro; IPR002890; A2M_N.
DR InterPro; IPR011625; A2M_N_2.
DR InterPro; IPR011627; A2M_Receptor.
DR InterPro; IPR000020; Anaphylatoxin.

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DR InterPro: IPR001840; Anaphylatoxin.
DR InterPro: IPR001599; MacroglobinA2.
DR InterPro: IPR001134; Netrin_C.
DR Pfam: PF00207; A2M; 1.
DR Pfam: PF07678; A2M_comp; 1.
DR Pfam: PF01835; A2M_N; 1.
DR Pfam: PF07703; A2M_N_2; 1.
DR Pfam: PF07677; A2M_recep; 1.
DR Pfam: PF01821; ANATO; 1.
DR Pfam: PF01759; NTR; 1.
DR PRINTS: PR00004; ANAPHYLATOXIN.
DR ProDom: PD003264; Anaphylatoxin; 1.
DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR PROSITE: PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE: PS01178; ANAPHYLATOXIN_2; 1.
DR PROSITE: PS0189; NTR; 1.
KW Complement alternate pathway; Complement pathway;
KW Direct protein sequencing; Glycoprotein; Immune response;
KW Inflammatory response; Innate immunity; Plasma; Signal;
KW Thioester bond.
FT SIGNAL 1 22 Complement C3.
FT CHAIN 23 1666 Complement C3 beta chain.
FT CHAIN 23 671 Complement C3 alpha chain.
FT CHAIN 676 1666 C3a anaphylatoxin.
FT PEPTIDE 676 753 Complement C3b alpha' chain.
FT CHAIN 754 1666 Complement C3d fragment.
FT CHAIN 993 1666 Anaphylatoxin-like.
FT DOMAIN 698 733 NTR.
FT DOMAIN 1522 1664 Poly-Arg.
FT COMPIAS 672 675 Poly-Leu.
FT COMPIAS 1242 1248 Cleavage (by C3 convertase).
FT SITE 753 754 Cleavage (by elastase).
FT SITE 992 993 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 944 944 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 1620 1620 Interchain (between beta and alpha chains) (By similarity).
FT DISULFID 557 821 By similarity.
FT DISULFID 630 666 By similarity.
FT DISULFID 698 725 By similarity.
FT DISULFID 699 732 By similarity.
FT DISULFID 712 733 By similarity.
FT DISULFID 878 1517 By similarity.
FT DISULFID 1106 1163 By similarity.
FT DISULFID 1363 1493 By similarity.
FT DISULFID 1394 1462 By similarity.
FT DISULFID 1510 1535 By similarity.
FT DISULFID 1522 1593 By similarity.
FT DISULFID 1540 1664 By similarity.
FT DISULFID 1640 1649 By similarity.
FT CROSSLNK 1015 1018 Isoglutamyl cysteine thioester (Cys-Gln).
FT CONFLICT 731 731 D -> N (in Ref. 3).
FT CONFLICT 1018 1018 Q -> E (in Ref. 4).
FT SEQUENCE 1666 AA; 166488 MW; 1C1F12199448FD49 CRC64;

Query Match 63.7%; Score 58; DB 1; Length 1666;
Best Local Similarity 62.5%; Pred. No. 1.5;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 KNRWEDFGQLYNVEA 16
Db 1222 KNRWEARQKLXSVEA 1237
|||||: :|||:|
|||||: :|||:|

RESULT 12
R1 ARATH STANDARD; PRT; 1399 AA.
ID R1 ARATH STANDARD; Q93VD0; Q94020; Q9FPP2;
AC Q9SAC6; Q93VD0; Q94020; Q9FPP2;
DT 01-FEB-2005 (Rel. 46, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Alpha-glucan water dikinase, chloroplast precursor (EC 2.7.9.4)
DE (starch-related R1 protein) (Starch excess protein 1).
GN Name=SEX1; Synonyms=R1; OrderedLocusNames=At1g10760;

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GN ORFNames=T16B5.10;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, SUBCELLULAR LOCATION,
RP DEVELOPMENTAL STAGE, AND MUTAGENESIS OF GLY-1268.
RX MEDLINE=21380420; PubMed=11487701; DOI=10.1105/tpc.13.8.1907;
RA Yu T.-S., Kofler H., Haeusel R.E., Hille D., Fluegge U.-I.,
RA Lue W.-L., Chen J., Weber A.;
RA Zeeman S.C., Smith A.M., Kossmann J., Lloyd J., Ritte G., Steup M.,
RT "The Arabidopsis sex1 mutant is defective in the R1 protein, a general
RT regulator of starch degradation in plants, and not in the chloroplast
RT hexose transporter."
RL Plant Cell 13:1907-1918(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712; DOI=10.1038/35048500;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Krenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vayberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana."
RL Nature 408:816-820(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 1220-1399.
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.D., Tripp C., Zhang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao Q., Choy N., Enju N., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Heuan V.W., Iida K., Karnes M.,
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kaniya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tamse R., Vayberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
RT genome."
RL Science 302:842-846(2003).
CC -!- FUNCTION: Mediates the incorporation of phosphate into starch-like
CC alpha-glucan. Acts as an overall regulator of starch mobilization.
CC Required for starch degradation, suggesting that the phosphate
CC content of starch regulates its degradability.
CC -!- CATALYTIC ACTIVITY: ATP + alpha-glucan + H(2)O = AMP + phospho-
CC alpha-glucan + phosphate.
CC -!- COFACTOR: Magnesium (By similarity).
CC -!- SUBCELLULAR LOCATION: Chloroplast; starch granules.
CC -!- DEVELOPMENTAL STAGE: The level of protein does not vary in a
CC circadian rhythm and is stable throughout day and night (at protein
CC level).
CC -!- SIMILARITY: Belongs to the PEP-utilizing enzyme family.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.

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AC	Q9MXA7;	
AD	01-OCT-2000 (TrEMBLrel. 15, Created)	
AE	01-OCT-2000 (TrEMBLrel. 15, last sequence update)	
AF	01-JUN-2003 (TrEMBLrel. 24, last annotation update)	
AG	MHC class I antigen (Fragment).	
AH	Name=Bain-UA*L13;	
AI	Barbus intermedius (Lake tana barbels).	
AJ	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AK	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
AL	Cyprinidae; Barbus.	
AM	NCBI_TaxID=40831;	
AN	[1]	
AO	NUCLEOTIDE SEQUENCE.	
AP	Kruiswijk C.P., Stet R.J.M.;	
AQ	Submitted (JUL/1998) to the EMBL/GenBank/DBJ databases.	
AR	EMBL; A0007897; CAB97341.1; -; Genomic_DNA.	
AS	HSP; P01897; ILDP.	
AT	GO; GO:0042612; C:MHC class I protein complex; IEA.	
AV	GO; GO:0030106; F:MHC class I receptor activity; IEA.	
AW	GO; GO:0013882; P:antigen presentation; IEA.	
AX	InterPro: IPR001039; MHC_I_alpha_A1A2.	
AY	pfam: PF00129; MHC_I_1.	
AZ	PRINTS; PR01638; MHCCLASSI.	
BA	1	
BB	NON_TER	
BC	92	
BD	SEQUENCE	
BE	92 AA; 10463 MW; A1D08F3030F9E144 CRC64;	
BF		
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BH		
BI		
BJ		
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BO		
BP		
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CT		

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 16:28:51 ; Search time 180 Seconds
(without alignments)
39.056 Million cell updates/sec

Title: US-09-865-281a-1

Perfect score: 91

Sequence: 1 KNRWEDPGKQLYNVEA 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 19975

Minimum DB seq length: 16

Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	100.0	16	4	Aab92360 Miscellan
2	91	100.0	16	6	Abp58217 Immunosti
3	91	100.0	16	8	Ad617594 Peptide d
4	91	100.0	16	9	Adv24825 CR2-bindl
5	38	41.8	16	2	Aaw32826 HIV-1 CDC
6	37	40.7	16	1	Aap82479 Peptide c
7	37	40.7	16	1	Aar24424 Sequence
8	37	40.7	16	2	Aar85369 HTLV-IIIB
9	37	40.7	16	2	Aaw07391 HIV-1 CD4
10	37	40.7	16	2	Aaw10345 HIV epit
11	37	40.7	16	2	Aaw16512 HTLV-IIIB
12	37	40.7	16	2	Aaw32824 HIV-1 SC
13	37	40.7	16	2	Aaw16535 HIV-1 BH1
14	37	40.7	16	2	Aaw32825 HIV-1 SF2
15	37	40.7	16	2	Aaw32822 HIV-1 BRU
16	37	40.7	16	2	Aaw32823 HIV-1 MN
17	37	40.7	16	2	Aaw32828 HIV-1 RF
18	37	40.7	16	2	Aaw53140 HIV gp160
19	37	40.7	16	2	Aaw85381 Helper T-
20	37	40.7	16	2	Aaw76982 Fusion im
21	37	40.7	16	2	Aaw54937 HIV gp120
22	37	40.7	16	2	Aay04046 Covalentl
23	37	40.7	16	3	Aay73159 HIV-deriv
24	37	40.7	16	4	Aab49073 HIV gp120

25	37	40.7	16	4	AAB46174	Aab46174 HIV gp120
26	37	40.7	16	4	AAU12518	Aau12518 Human HIV
27	37	40.7	16	4	AAU12526	Aau12526 Human HIV
28	37	40.7	16	4	AAU12495	Aau12495 Human HIV
29	37	40.7	16	4	AAU12540	Aau12540 Human HIV
30	37	40.7	16	4	ABP25338	Abp25338 HTL cadid
31	37	40.7	16	4	ABP25261	Abp25261 HIV HLA-D
32	37	40.7	16	4	ABP25382	Abp25382 HIV-1 epi
33	37	40.7	16	5	AAW49301	Aam49301 CD4 pepti
34	37	40.7	16	5	AAE20151	Aae20151 Human imm
35	37	40.7	16	6	ABG72720	Abg72720 HIV-1 gp1
36	37	40.7	16	6	ABU87175	Abu87175 HIV T cel
37	37	40.7	16	7	ADA49515	Ada49515 Multi-epl
38	37	40.7	16	7	ADC09978	Adc09978 HIV gp120
39	37	40.7	16	7	ADW36356	Adw36356 HLA bindi
40	37	40.7	16	7	ADW36078	Adw36078 HLA bindi
41	37	40.7	16	7	ADW35909	Adw35909 HLA bindi
42	37	40.7	16	7	ADW33657	Adw33657 HLA bindi
43	37	40.7	16	7	ADW34890	Adw34890 HLA bindi
44	37	40.7	16	8	ADO24193	Ado24193 HIV epit
45	37	40.7	16	8	ADP02878	Adp02878 HIV gp120

ALIGNMENTS

RESULT 1

AAB92360

ID AAB92360 standard; peptide; 16 AA.

XX AAB92360;

XX 22-JUN-2001 (first entry)

DE Miscellaneous peptide SEQ ID NO:1536.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013576.

PR 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

PR 15-OCT-1999; 99US-0159783P.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.

XX Disclosure; Page 707; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)

XX comprising a therapeutically active amino acid region (III) and a
XX reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
XX a less therapeutically active amino acid region (IV), which covalently
XX bonds with amino/hydroxyl/thiol groups on blood components to form a
XX peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth
XX factors and neurotransmitters, to protect them from peptidase activity in
XX vivo for the treatment of various disorders. Endogenous therapeutic

CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 16 AA;

Query Match 100.0%; Score 91; DB 4; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.5e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKOLYNVEA 16
 DB 1 KNRWEDPGKOLYNVEA 16
 |||||

RESULT 2
 ABP58217
 ID ABP58217 standard; peptide; 16 AA.
 XX
 AC ABP58217;
 XX
 DT 21-MAR-2003 (first entry)
 XX
 DE Immunostimulant C3d peptide.
 XX
 KW Immunostimulant; C3d; human; fusion protein; tumour; vaccine; adjuvant.
 XX
 OS Homo sapiens.
 XX
 PN WO200297041-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 29-MAY-2002; 2002WO-US016651.
 XX
 PR 29-MAY-2001; 2001US-00865281.
 XX
 PA (IMMP-) IMMIPHERON INC.
 PA (INNE-) INNEXUS CORP.
 XX
 PI Kohler H, Morgan C;
 XX
 WPI; 2003-140458/13.
 XX
 PT Novel fusion protein for use as molecular adjuvant, has an antibody and a
 PT peptide with immunostimulatory, membrane transport or homophilic
 PT activities, connected to the antibody by peptide bonds.
 XX
 PS Example 1; Page 14; 39pp; English.
 XX
 CC The present invention provides a fusion protein made up of an antibody
 CC and a peptide having e.g. immunostimulant, membrane transport or
 CC homophilic activity. The peptide is located at a site in the antibody
 CC such that it does not compromise the antigen recognition of the antibody.
 CC In order to enhance its activity, the peptide may be flanked by loop-
 CC forming or conformation-conferring sequences. The present sequence is an
 CC example of a suitable immunostimulatory peptide for use as a fusion
 CC protein component. The peptide is derived from human C3d amino acids 1217
 CC -1232. In examples from the invention, the C3d peptide was affinity cross
 CC -linked to tumour anti-idiotypic and tumour idiotype vaccine antibodies,
 CC significantly enhancing the immune response to the tumour and protecting
 CC against tumour challenge. The vaccination protocol did not include any
 CC adjuvant, such as Freund's adjuvant or keyhole limpet haemocyanin
 CC conjugation, both of which are not permissible by the FDA for human use
 XX
 SQ Sequence 16 AA;

Query Match 100.0%; Score 91; DB 6; Length 16;

Best Local Similarity 100.0%; Pred. No. 6.5e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKOLYNVEA 16
 DB 1 KNRWEDPGKOLYNVEA 16
 |||||

RESULT 3
 ADS17594
 ID ADS17594 standard; peptide; 16 AA.
 XX
 AC ADS17594;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Peptide derived from the C3d peptide and affinity linked to 3H1 antibody.
 XX
 KW immunostimulatory; membrane transport; homophilic; signaling protein;
 KW caspase; kinase; phosphatase; viral protein; tumour antigen;
 KW nuclear protein; nucleolar protein; DNA synthesis; cytoskeletal protein;
 KW cell proliferation; cytoskeleton; membrane transporter peptide;
 KW Kaposi fibroblast factor; TAT peptide; HIV-1; antenapedia homeodomain;
 KW herpes virus protein VP22; transportan peptide; Alzheimer's disease;
 KW Huntington's disease; Parkinson's disease; C3d; 3H1; monoclonal antibody;
 KW anti-idiotypic antibody; carcino-embryonic antigen; CEA;
 KW anti-idiotypic vaccine; antibody.
 XX
 OS Synthetic.
 XX
 PN WO2004078146-A2.
 XX
 PD 16-SEP-2004.
 XX
 PF 05-MAR-2004; 2004WO-US006911.
 XX
 PR 05-MAR-2003; 2003US-0451980P.
 XX
 PA (INNE-) INNEXUS BIOTECHNOLOGY INC.
 PA (IMMP-) IMMIPHERON INC.
 XX
 PI Kohler H, Muller S, Brown TL, Zhao Y, Morgan AC;
 XX
 WPI; 2004-653567/63.
 XX
 PT New compound for regulating normal or infected cell function comprising
 PT an antibody conjugated to a membrane transporter peptide, useful in
 PT preparing a composition for treating or preventing human diseases, e.g.
 PT Alzheimer's disease.
 XX
 PS Example 1; SEQ ID NO 1; 50pp; English.
 XX
 CC The specification describes a fusion protein for regulating normal or
 CC infected cell function, comprising an antibody conjugated to a peptide
 CC having immunostimulatory, membrane transport, and homophilic activities.
 CC The antibody is immunospecific for a signaling protein internal cell
 CC consisting of caspases, kinases or phosphatases, an immature viral
 CC protein, a cell-surface or intracellular tumour antigen, a nuclear or
 CC nucleolar protein participating in regulation of DNA synthesis and gene
 CC expression, or a cytoskeletal protein participating in cell proliferation
 CC or cytoskeleton. The peptide portion of the fusion protein is preferably a
 CC membrane transporter peptide that is endogenous to Kaposi fibroblast
 CC factor, TAT peptides of HIV-1, antenapedia homeodomain-derived peptide,
 CC herpes virus protein VP22, or transportan peptide. Fusion protein of the
 CC invention are useful for preparing a composition for treating or
 CC preventing human diseases, e.g., Alzheimer's disease, Huntington's
 CC disease or Parkinson's disease. The present sequence represents a peptide
 CC derived from the C3d region 1217-1232, which was affinity cross-linked
 CC with 3H1 monoclonal antibody to produce fusion proteins of the invention.
 CC 3H1 is a murine anti-idiotypic antibody which mimics the carcino-
 CC embryonic antigen (CEA), and induces anti-CEA antibodies. The resulting
 CC C3d-3H1 fusion protein was used to enhance an anti-idiotypic vaccine.
 XX

SQ Sequence 16 AA;

Query Match 100.0%; Score 91; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.5e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKQLYNVEA 16
 |||||
 DB 1 KNRWEDPGKQLYNVEA 16

RESULT 4
 ADV24825
 ID ADV24825 standard; peptide; 16 AA.
 AC ADV24825;
 XX
 DT 24-FEB-2005 (first entry)
 XX
 DE CR2-binding complement C3d peptide, SEQ ID NO:2.
 XX
 KW Multivalent ligand; cell signaling; diagnostic; decontamination;
 KW autoimmune disease; immune disorder; cancer; neoplasm; cancer metastasis;
 KW immunosuppressive; immunomodulator; cytostatic; complement C3d.
 XX
 OS Unidentified.
 XX
 PN US2004248801-A1.
 XX
 PD 09-DEC-2004.
 XX
 PF 22-MAR-2004; 2004US-00806056.
 XX
 PR 21-MAR-2000; 2000US-0191014P.
 PR 21-MAR-2001; 2001US-00815296.
 PR 21-MAR-2003; 2003US-0456778P.
 XX
 PA (KIES/) KIESSLING L L.
 PA (GRIF/) GRIFFITH B R.
 PA (GEST/) GESTWICKI J E.
 PA (STRO/) STRONG L.
 XX
 PI Kiessling LL, Griffith BR, Gestwicki JE, Strong L;
 XX
 XX WPI; 2005-046763/05.
 XX
 DR Novel multivalent ligand, useful for inducing biological response,
 PT enhancing aggregation of biological particles and enhancing induction of
 PT cellular response.
 XX
 PS Example 3; SEQ ID NO 2; 76pp; English.
 XX
 CC The invention relates to a multivalent ligand comprising a plurality of
 CC signal recognition elements (SRE), binding recognition elements (BRE) and
 CC functional elements (FE), and which is bonded to a polymeric scaffold.
 CC The SREs are involved, either directly or indirectly, in biological
 CC signaling processes, while the BREs facilitate the binding associated
 CC with the process. Examples of SREs used in the multivalent ligand include
 CC epitopes (especially one characteristic of a cancer cell), antigens,
 CC antibodies or fragments thereof, cell surface receptors, polysaccharides,
 CC nucleic acids or small drug-like compounds, and suitable BREs include
 CC polysaccharides or metal-chelating groups which are optionally bound to
 CC metals. The FE may be a detectable label, a reporter group or an enzyme.
 CC The invention also relates to use of multivalent ligands in a method for
 CC inducing a biological response in a biological system such as a cell or
 CC organism which comprises one or more receptors recognized by an SRE; a
 CC method of enhancing aggregation of biological particles such as cells or
 CC viruses using a multivalent ligand complex which comprises several
 CC recognition elements which each induce aggregation of one or more of the
 CC biological particles; a method for inducing a cellular response or for
 CC enhancing cellular response induction using a multivalent ligand; a
 CC method of generating an assembly of biological macromolecules or
 CC particles by providing a multivalent ligand comprising a molecular

CC scaffold to which several biological macromolecules or particles are
 CC attached via BREs, wherein the number, density and spacing of the BREs is
 CC controlled; and a library of multivalent ligands of the invention, in
 CC which the members of the libraries vary in the type, number and/or
 CC relative positioning of recognition elements, the combinations of BREs
 CC and SREs present, the presence and/or positioning of spacers, the number
 CC of repeating units or monomers, and the presence, type or number of FEs.
 CC The invention also discloses pharmaceutical compositions comprising
 CC multivalent ligands of the invention. The multivalent ligands are useful
 CC for modulating immune system cell responses to epitopes, thereby
 CC inhibiting or attenuating autoimmune disorders, and are also useful for
 CC treating undesired cell proliferation (cancer) and undesired cell
 CC migration (metastasis). They can be used in diagnostic applications for
 CC the detection of biological molecules or particles in biological systems,
 CC and are useful for preventing or inhibiting biofouling or removing
 CC undesired cells in a selected environment. The present sequence
 CC represents a complement C3d peptide able to bind complement receptor CR2
 CC which may be used as a signal in a multivalent ligand for inducing an
 CC enhanced immune response.
 XX
 SQ Sequence 16 AA;

Query Match 100.0%; Score 91; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.5e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNRWEDPGKQLYNVEA 16
 |||||
 DB 1 KNRWEDPGKQLYNVEA 16

RESULT 5
 AAW32826
 ID AAW32826 standard; peptide; 16 AA.
 XX
 AC AAW32826;
 XX
 DT 17-OCT-2003 (revised)
 DT 14-JAN-1998 (first entry)
 XX
 DE HIV-1 CDC4 envelope glycoprotein 120 T cell epitope T1.
 XX
 KW Hydrophilic; antigenic determinant; HIV; envelope; glycoprotein; env; gp;
 KW recognition; B lymphocyte; type specific; antibody; vaccine; protection;
 KW immune response; infection; neutralisation; epitope.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO9714436-A1.
 XX
 PD 24-APR-1997.
 XX
 PF 18-OCT-1996; 96WO-US016911.
 XX
 PR 20-OCT-1995; 95US-00546515.
 PR 09-FEB-1996; 96US-00599266.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Haynes BF, Palker TV;
 XX
 XX WPI; 1997-244862/22.
 XX
 PT Synthetic human immunodeficiency virus vaccine - comprising hydrophilic
 PT peptide corresponding to at least 1 antigenic determinant of envelope
 PT glyco:protein recognised by B lymphocytes.
 XX
 PS Disclosure; Page 23; 104pp; English.
 XX
 CC An essentially pure hydrophilic peptide, comprising at least 1 antigenic
 CC determinant of human immunodeficiency virus (HIV) envelope (env)
 CC glycoprotein (gp) recognised by B lymphocytes, when covalently linked to
 CC a carrier molecule, i.e. the present sequence, induces the production of

CC high titres of protective, type specific anti-HIV antibodies (Ab) in a
 CC mammal. The peptide can be used in vaccines for producing a protective
 CC immune response to HIV infection, while a HIV neutralising Ab can be
 CC induced in a primate by administering a composition comprising HIV env
 CC peptides that disrupt gp120/gp41 interactions. (Updated on 17-OCT-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 16 AA;

Query Match 41.8%; Score 38; DB 2; Length 16;
 Best Local Similarity 54.5%; Pred. No. 96;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLY 12
 |||: ||:|
 Db 5 NRQVGVKAMY 15

RESULT 6
 AAP82479
 ID AAP82479 standard; protein; 16 AA.

XX AAP82479;

XX 25-MAR-2003 (revised)
 DT 12-NOV-1990 (first entry)

XX Peptide component of AIDS vaccine.

DE AIDS vaccine; T-cells.

XX Synthetic.

XX EP273716-A.

XX 06-JUL-1988.

XX 23-DEC-1987; 87BP-00311391.

XX 30-DEC-1986; 86US-00947935.

PR 12-FEB-1987; 87US-00014430.

XX (USDC) US SEC OF COMMERCE.

PA (USSH) US DEPT HEALTH & HUMAN SERVICE.

XX Delisi C, Margalit H, Cornette JL, Ouyang CS;

XX WPI; 1988-184640/27.

XX Synthetic peptide(s) as vaccines for AIDS - selected from peptide regions
 PT which can fold as a maximally amphipathic helix recognised by T cells.

XX Claim 9; Page 10; 16pp; English.

XX This peptide is a component of an AIDS vaccine. It can fold as a
 CC maximally amphipathic helix and is recognised by T-cells immune to the
 CC AIDS virus envelope protein. See also AAP82462-78. (Updated on 25-MAR-
 CC 2003 to correct PA field.)
 XX

SQ Sequence 16 AA;

Query Match 40.7%; Score 37; DB 1; Length 16;
 Best Local Similarity 45.5%; Pred. No. 1.4e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLY 12
 |||: ||:|
 Db 5 NRQVGVKAMY 15

RESULT 7
 AAR24424
 ID AAR24424 standard; peptide; 16 AA.

XX AAR24424;
 AC 25-MAR-2003 (revised)
 XX 21-NOV-1992 (first entry)
 DT
 DE Sequence of T helper peptide of gp120 at amino acid residue numbers 105-
 DE 117(172).

XX Vaccine; AIDS; HIV-1; carrier peptide.

XX Homo sapiens.

XX WO9208491-A1.

XX 29-MAY-1992.

XX 19-NOV-1991; 91WO-US008653.

XX 20-NOV-1990; 90US-00616247.

XX (TANO-) TANOX BIOSYSTEMS INC.

XX Chang TW, Fung MSC;

XX WPI; 1992-199955/24.

XX Vaccines comprising anti-idiotype antibody conjugates - induce prodn. of
 PT neutralising antibodies against HIV-1 for immunisation against HIV
 PT infection and AIDS.

XX Claim 12; Page 26 and page 15; 29pp; English.

XX The invention includes epitope-directed immunization with a vaccine in
 CC which an anti-idiotype antibody is conjugated to a carrier, which can be
 CC either a protein or its derived T helper peptide. The carrier is one
 CC against which the vaccine recipient has previously immunized or otherwise
 CC previously exposed, or which enhances the immune response against the
 CC anti-idiotype antibody. One exemplary anti-idiotype antibody which
 CC induces antibodies against the PND is AB19-4. Where the anti-idiotype
 CC induces Ab3 against HIV-1, the carrier preferably is HBsAg or HIV-1 p24,
 CC or a peptide of either HBsAg or HIV-1 p24 including a T helper
 CC determinant. "PND" = the principal neutralizing determinant ("PND") of
 CC gp120. A T-helper peptide with the sequence in AAR24423, or immunological
 CC equivalents of this sequence is suitable for conjugation with AB19-4 or
 CC other anti-idiotypes which induce Ab3 against HIV-1. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX

SQ Sequence 16 AA;

Query Match 40.7%; Score 37; DB 2; Length 16;
 Best Local Similarity 45.5%; Pred. No. 1.4e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLY 12
 |||: ||:|
 Db 6 NRQVGVKAMY 16

RESULT 8

AAR85369

ID AAR85369 standard; peptide; 16 AA.

XX AAR85369;

XX 16-OCT-2003 (revised)

DT 12-JUN-1996 (first entry)

XX HTLV-IIIb gp120 envelope T cell epitope T1.

XX Human immunodeficiency virus; HIV; HTLV-IIIb; envelope; glycoprotein;
 KW hydrophilic; immunisation; antibody production; fusion peptide; SP-10;
 KW conjugate; carrier.

XX OS Human immunodeficiency virus 1.
 XX PN WO9529700-A1.
 XX PD 09-NOV-1995.
 XX PF 28-APR-1995; 95WO-US0005465.
 XX PR 29-APR-1994; 94US-00235305.
 XX PA (UYDU-) UNIV DUKE.
 XX PI Haynes BF, Palker TJ;
 XX DR WPI; 1995-392926/50.
 XX PT New peptide(s) corresponding to HIV sequences - used for inducing
 PT protective immunity to HIV and in the treatment of e.g. auto-immune
 PT disease, infectious disease or tumours.
 XX PS Claim 6; Page 16; 128pp; English.
 XX CC AAR85369 and AAR85370 are HTLV-IIIB gp120 envelope T cell epitopes T1 and
 CC T2. The two peptides corresp. to amino acids 428-443 and 112-124 of the
 CC HIV isolate, HTLV-IIIB gp120 envelope protein. The peptides can be
 CC conjugated to SP-10 and "SP-10-like" regions of other HIV isolates.
 CC Conjugates produced are capable of inducing the production of high titres
 CC of protective, type-specific, anti-HIV antibodies. Helper T cells and
 CC cytotoxic T cells are also activated by the peptide immunogens. (Updated
 CC on 16-OCT-2003 to standardise OS field)
 XX SQ Sequence 16 AA;
 Query Match 40.7%; Score 37; DB 2; Length 16;
 Best Local Similarity 45.5%; Pred. No. 1.4e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 2 NRWEDPGKQLY 12
 DB 5 NMWQEVGKAMY 15
 RESULT 9
 AAW07391
 ID AAW07391 standard; peptide; 16 AA.
 XX AC AAW07391;
 XX XX 16-OCT-2003 (revised)
 DT 24-FEB-1997 (first entry)
 XX DE HIV-1 CD4 binding site.
 XX KW HIV-1; gp120; V3 loop; common consensus PND domain; envelop; CD4;
 KW binding site; stem-loop; lysine branched peptide; AIDS.
 XX OS Human immunodeficiency virus 1.
 XX JP08231423-A.
 XX PD 10-SEP-1996.
 XX PF 27-FEB-1995; 95JP-00038835.
 XX PR 27-FEB-1995; 95JP-00038835.
 XX PA (TERU) TERUMO CORP.
 XX PA (OKUD/) OKUDA K.
 XX DR WPI; 1996-461278/46.
 XX PT Novel AIDS vaccine - comprises branched lysine peptide fragments derived

PT from HIV env protein.
 XX PS Example 1; Page 5; 8pp; Japanese.
 XX CC This is the CD4 binding site sequence from HIV-1. Part of the peptide
 CC (from residues 4-16) was fused to part of the HIV-1 gp120 V3 loop common
 CC consensus PND sequence (AAW07390) to form a stem-loop construct
 CC (AAW07395). This construct was used with the V3 loop sequences from HIV-
 CC 12 strains IIIB (AAW07392), Thai B (AAW07393) or HGP-30 (AAW07394) to
 CC generate a lysine branched peptide which is useful for the prevention and
 CC treatment of AIDS. (Updated on 16-OCT-2003 to standardise OS field)
 XX SQ Sequence 16 AA;
 Query Match 40.7%; Score 37; DB 2; Length 16;
 Best Local Similarity 45.5%; Pred. No. 1.4e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 2 NRWEDPGKQLY 12
 DB 5 NMWQEVGKAMY 15
 RESULT 10
 AAW10345
 ID AAW10345 standard; peptide; 16 AA.
 XX AC AAW10345;
 XX DT 15-OCT-1997 (first entry)
 XX DE HIV epitope env T1 amino acid residues 428-443 of gp120.
 XX KW Human immunodeficiency virus type-1; HIV-1; T cell response; detection;
 KW peripheral blood mononuclear cell; PBMC.
 XX OS Synthetic.
 XX PN WO9641189-A1.
 XX PD 19-DEC-1996.
 XX PF 07-JUN-1996; 96WO-US010108.
 XX PR 07-JUN-1995; 95US-00488435.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Shearer GM, Berzofsky JA, Clerici M;
 XX DR WPI; 1997-108658/10.
 XX PT Diagnosis of exposure to infectious agents, partic. HIV - by detecting
 PT activation of peripheral blood mononuclear cells from patient by epitope
 PT of infectious agent.
 XX PS Claim 15; Page 62; 82pp; English.
 XX CC The present sequence represents a synthetic HIV-1 gp120 peptide env T1
 CC for use in a method for diagnosing exposure of a patient to human
 CC immunodeficiency virus (HIV). The method involves: (a) obtaining
 CC peripheral blood mononuclear cells (PBMC) from a patient; (b) incubating
 CC the PBMC with at least 1 synthetic peptide representing an epitope(s) of
 CC the infectious agent (e.g. the present sequence); and (c) determining the
 CC activation of the PBMC as a result of the incubation in step (b). The
 CC method can provide for the early detection of exposure to infectious
 CC organisms, specifically HIV in this case. The method can be used to
 CC assess exposure to HIV without concomitant infection. It also provides an
 CC earlier identification of HIV exposure, than is provided by
 XX SQ Sequence 16 AA;

CC induced in a primate by administering a composition comprising HIV env
CC peptides that disrupt gp120/gp41 interactions. (Updated on 17-Oct-2003 to
CC standardise OS field)

xx

SQ Sequence 16 AA;

Query Match 40.7%; Score 37; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLY 12

Db 5 NMWQEVGKANY 15

Search completed: May 15, 2006, 16:34:34
Job time : 182 secs

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OM protein - protein search, using sw model

Run on: May 15, 2006, 16:39:16 ; Search time 45 Seconds
(without alignments)
29.396 Million cell updates/sec

Title: US-09-865-281A-1

Perfect score: 91

Sequence: 1 KNREDPGKQLYNVEA 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 7712

Minimum DB seq length: 16

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: /cgn2_6/prodata/1/iaa/5.COMB.pep.*

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3: /cgn2_6/prodata/1/iaa/H.COMB.pep.*

4: /cgn2_6/prodata/1/iaa/PCUS.COMB.pep.*

5: /cgn2_6/prodata/1/iaa/RE.COMB.pep.*

6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	100.0	16	US-09-070-907-1	Sequence 1, Appli
2	91	100.0	16	US-09-623-548A-1536	Sequence 1536, Ap
3	91	100.0	16	US-09-657-276-1536	Sequence 1536, Ap
4	37	40.7	16	US-08-213-124-5	Sequence 5, Appli
5	37	40.7	16	US-08-488-252-35	Sequence 35, Appl
6	37	40.7	16	US-07-847-311A-15	Sequence 15, Appl
7	37	40.7	16	US-09-046-373-1	Sequence 1, Appli
8	37	40.7	16	US-09-009-953-230	Sequence 230, App
9	37	40.7	16	US-09-340-798A-40	Sequence 40, Appl
10	37	40.7	16	US-09-311-784A-308	Sequence 308, App
11	37	40.7	16	US-09-724-961-51	Sequence 51, Appl
12	37	40.7	16	US-09-580-018-51	Sequence 51, Appl
13	37	40.7	16	US-09-724-551-51	Sequence 51, Appl
14	37	40.7	16	US-09-862-849-1	Sequence 1, Appli
15	37	40.7	16	US-10-114-716A-1	Sequence 1, Appli
16	37	40.7	16	US-09-724-953-9	Sequence 9, Appli
17	37	40.7	16	US-09-724-567-9	Sequence 9, Appli
18	37	40.7	16	US-09-724-940-51	Sequence 51, Appl
19	37	40.7	16	US-09-579-952-9	Sequence 9, Appli
20	37	40.7	16	US-09-585-817-9	Sequence 9, Appli
21	29	31.9	16	US-08-257-528B-22	Sequence 22, Appl
22	29	31.9	16	US-08-460-602A-22	Sequence 22, Appl
23	29	31.9	16	US-08-463-966A-22	Sequence 22, Appl
24	29	31.9	16	US-08-465-217A-22	Sequence 22, Appl
25	29	31.9	16	US-08-464-329A-22	Sequence 22, Appl
26	29	31.9	16	US-08-462-507A-22	Sequence 22, Appl
27	29	31.9	16	US-08-467-881A-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1

US-09-070-907-1

; Sequence 1, Application US/09070907

; Patent No. 6238667

; GENERAL INFORMATION:

; APPLICANT: Kohler, Heinz

; TITLE OF INVENTION: METHOD OF AFFINITY CROSS-LINKING BIOLOGICALLY ACTIVE

; FILE REFERENCE: 35629

; CURRENT APPLICATION NUMBER: US/09/070,907

; CURRENT FILING DATE: 1998-05-04

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: Patent In Ver. 2.0 - beta

; SEQ ID NO 1

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: AMINO ACID

; OTHER INFORMATION: SEQUENCE DERIVED FROM Cds3 peptide

US-09-070-907-1

Query Match 100.0%; Score 91; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 7.4e-09; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNREDPGKQLYNVEA 16

|||||

Db 1 KNREDPGKQLYNVEA 16

RESULT 2

US-09-623-548A-1536

; Sequence 1536, Application US/09623548A

; Patent No. 6849714

; GENERAL INFORMATION:

; APPLICANT: Conjuchem, Inc.

; APPLICANT: Bridon, Dominique

; APPLICANT: Ezrin, Alan

; APPLICANT: Milner, Peter

; APPLICANT: Holmes, Darren

; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM

; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD

; FILE REFERENCE: 2110

; CURRENT APPLICATION NUMBER: US/09/623,548A

; CURRENT FILING DATE: 2000-09-05

; PRIOR APPLICATION NUMBER: 60/134,406

; PRIOR FILING DATE: 1999-05-17

; PRIOR FILING DATE: 1999-05-17

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; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1536
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-1536

Query Match      100.0%; Score 91; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.4e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWDPGKQLYNVEA 16
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Db 1 KNRWDPGKQLYNVEA 16

RESULT 3
US-09-657-276-1536
; Sequence 1536, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1536
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-1536

Query Match      100.0%; Score 91; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.4e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWDPGKQLYNVEA 16
| | | | | | | | | | | | | | | |
Db 1 KNRWDPGKQLYNVEA 16

RESULT 4
US-08-213-124-5
; Sequence 5, Application US/08213124
; Patent No. 5693325
; GENERAL INFORMATION:
; APPLICANT: Kahn, Michael
```

```
; TITLE OF INVENTION: PEPTIDE VACCINES AND METHODS RELATING
; TITLE OF INVENTION: THEREO
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/213,124
; FILING DATE: 15-MAR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Hermanns, Karl R.
; REGISTRATION NUMBER: 33,507
; REFERENCE/DOCKET NUMBER: 670063.411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANDBERRY
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-213-124-5

Query Match      40.7%; Score 37; DB 1; Length 16;
Best Local Similarity 45.5%; Pred. No. 11;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNRWDPGKOLY 12
| | : | : | : |
Db 5 NNRWQEVGKAMY 15

RESULT 5
US-08-488-252-35
; Sequence 35, Application US/08488252
; Patent No. 5763160
; GENERAL INFORMATION:
; APPLICANT: Chang Yi Wang
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND PROCESS
; TITLE OF INVENTION: OF USING SAME FOR THE DETECTION OF ANTIBODIES TO
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS (HIV) GPI20 ENVELOPE
; TITLE OF INVENTION: PROTEIN, DIAGNOSIS OF AIDS AND PRE-AIDS CONDITIONS
; TITLE OF INVENTION: AND AS VACCINES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVE.
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; OPERATING SYSTEM: IBM PC COMPATIBLE
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,252
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08\326,676
FILING DATE: 07-Jun-1995
APPLICATION NUMBER: 07\726,605
FILING DATE: 09-July-1991
APPLICATION NUMBER: 07\663,262
FILING DATE: 01-Mar-1991
APPLICATION NUMBER: 07\155,321
FILING DATE: 12-Feb-1988
ATTORNEY/AGENT INFORMATION:
NAME: Maria C. H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4004 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: Amino acids
STRANDEDNESS:
TOPOLOGY: Unknown
US-08-488-252-35

Query Match 40.7%; Score 37; DB 1; Length 16;
Best Local Similarity 45.5%; Pred. No. 11;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
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Db 5 NMWQEVGKAMY 15

RESULT 6

US-07-847-311A-15
Sequence 15, Application US/07847311A
Patent No. 5976541
GENERAL INFORMATION:
APPLICANT: Berzofsky, Jay A.
APPLICANT: Takeshita, Toshiyuki
APPLICANT: Shirai, Mutsunori
APPLICANT: Pendleton, C.D.
APPLICANT: Koslowski, Steven
APPLICANT: Margulies, David H.
TITLE OF INVENTION: Potent Peptide for Stimulation of
CYTOTOXIC T LYMPHOCYTES SPECIFIC FOR THE HIV-1 ENVELOPE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolaash & Birch
STREET: 301 N. Washington
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/847,311A
FILING DATE: 06-MAR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1173-392P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Human Immunodeficiency Virus Type I
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..16
OTHER INFORMATION: /label= peptide
OTHER INFORMATION: /note= "peptide T1, T-cell helper determinant in
HIV-1 envelope glycoprote..."
US-07-847-311A-15

Query Match 40.7%; Score 37; DB 1; Length 16;
Best Local Similarity 45.5%; Pred. No. 11;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
|::||:|
Db 5 NMWQEVGKAMY 15

RESULT 7

US-09-046-373-1
Sequence 1, Application US/09046373
Patent No. 6235714
GENERAL INFORMATION:
APPLICANT: Sudhir Paul
APPLICANT: Larry J. Smith
APPLICANT: Gennady Gololobov
TITLE OF INVENTION: Methods for Identifying Inducers and
INHIBITORS OF CATALYTIC ANTIBODIES, COMPOSITIONS AND THEIR
USE
TITLE OF INVENTION: Use
FILE REFERENCE: UNMC 63123
CURRENT APPLICATION NUMBER: US/09/046,373
CURRENT FILING DATE: 1998-03-23
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 16
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus-1
US-09-046-373-1

Query Match 40.7%; Score 37; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 11;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
|::||:|
Db 5 NMWQEVGKAMY 15

RESULT 8

US-09-009-953-230
Sequence 230, Application US/09009953
Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
REACTIVE DR RESTRICTED EPITOPES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

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;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/009,953
;   FILING DATE: 21-Jan-1998
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/036,713
;   FILING DATE: 23-JAN-1997
;   APPLICATION NUMBER: US 60/037,432
;   FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Weber, Ellen Lauver
;   REGISTRATION NUMBER: 32,762
;   REFERENCE/DOCKET NUMBER: 018623-011520US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-576-0200
;   TELEFAX: 415-576-0300
;   TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 230:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 16 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 230:
US-09-009-953-230

Query Match      40.7%; Score 37; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 11;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      2 NRWEDPGKQLY 12
      ||: ||: ||: ||:
Db      6 NMWQEVGKAMY 16

RESULT 9
US-09-340-798A-40
; Sequence 40, Application US/09340798A
; Patent No. 6534312
; GENERAL INFORMATION:
;   APPLICANT: SHIVER, JOHN W.
;   LIU, MARGARET A.
;   PERRY, HELEN C.
;   DAVIES, MARY-ELLEN M.
;   FREED, DANIEL C.
; TITLE OF INVENTION: VACCINES COMPRISING SYNTHETIC GENES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
;   STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
;   CITY: RAHWAY
;   STATE: NEW JERSEY
;   COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/340,798A
;   FILING DATE: 28-Jun-1999
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/877,418
;   FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: HAND, J. MARK
;   REGISTRATION NUMBER: 36,545
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;
; REFERENCE/DOCKET NUMBER: 19729Y
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 908-594-3905
;   TELEFAX: 908-594-4720
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 16 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-340-798A-40

Query Match      40.7%; Score 37; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 11;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      2 NRWEDPGKQLY 12
      ||: ||: ||: ||:
Db      5 NMWQEVGKAMY 15

RESULT 10
US-09-311-784A-308
; Sequence 308, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
;   APPLICANT: Fikes, John D.
;   APPLICANT: Hermanson, Gary G.
;   APPLICANT: Sette, Alessandro
;   APPLICANT: Ishioka, Glenn Y.
;   APPLICANT: Livingston, Brian
;   APPLICANT: Chesnut, Robert W.
;   APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
;   IMMUNE RESPONSE AND METHODS OF USING THE SAME
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HIV1 ENV 566 (peptide F091.15)
US-09-311-784A-308

Query Match      40.7%; Score 37; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 11;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      2 NRWEDPGKQLY 12
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Db      6 NMWQEVGKAMY 16

RESULT 11
US-09-724-961-51
; Sequence 51, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
;   APPLICANT: Schenk, Dale B.
;   APPLICANT: Bard, Frederique
;   APPLICANT: Vasquez, Nicki
;   APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
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; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HIV gp120 T1
; OTHER INFORMATION: universal T-cell epitope
US-09-724-961-51

Query Match          40.7%; Score 37; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 11;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
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Db 5 NMWQEVGKAMY 15

RESULT 12
US-09-580-018-51
; Sequence 51, Application US/095800018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HIV gp120 T1
; OTHER INFORMATION: universal T-cell epitope
US-09-580-018-51

Query Match          40.7%; Score 37; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 11;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
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Db 5 NMWQEVGKAMY 15

RESULT 13
US-09-724-551-51
; Sequence 51, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
```

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; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HIV gp120 T1
; OTHER INFORMATION: universal T-cell epitope
US-09-724-551-51

Query Match          40.7%; Score 37; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 11;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
   ||: ||: ||
Db 5 NMWQEVGKAMY 15

RESULT 14
US-09-862-849-1
; Sequence 1, Application US/09862849
; Patent No. 6855528
; GENERAL INFORMATION:
; APPLICANT: Sudhir Paul
; APPLICANT: Larry J. Smith
; APPLICANT: Gennady Gololobov
; TITLE OF INVENTION: Methods for Identifying Inducers and Inhibitors of Proteolytic
; TITLE OF INVENTION: Antibodies, Compositions and Their Uses
; FILE REFERENCE: UNMC 63123 DIV
; CURRENT APPLICATION NUMBER: US/09/862,849
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/046,373
; PRIOR FILING DATE: 1998-03-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus-1
; OTHER INFORMATION:
US-09-862-849-1

Query Match          40.7%; Score 37; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 11;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
   ||: ||: ||
Db 5 NMWQEVGKAMY 15

RESULT 15
US-10-114-716A-1
; Sequence 1, Application US/10114716A
; Patent No. 6855804
; GENERAL INFORMATION:
; APPLICANT: Sudhir Paul
; APPLICANT: Yasuhiro Nishiyama
; TITLE OF INVENTION: Covalently Reactive Transition State
; TITLE OF INVENTION: Analogs and Methods of Use Thereof
; FILE REFERENCE: UTH001HB
; CURRENT APPLICATION NUMBER: US/10/114,716A
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; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 09/862,849
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/046,373
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 60/280,624
; PRIOR FILING DATE: 2001-03-31
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus-1
US-10-114-716A-1

Query Match      40.7% Score 37; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 11;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      2 NRWEDPGKQLY 12
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Db      5 NMWQEVGKAMY 15
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Search completed: May 15, 2006, 16:40:32
Job time : 46 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 16:50:07 ; Search time 159 Seconds
(without alignments)
42.046 Million cell updates/sec

Title: US-09-865-281A-1

Perfect score: 91

Sequence: 1 KNWEDPGKQLYNVEA 16

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 11256

Minimum DB seq length: 16

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA_Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	91	100.0	16	5	US-10-795-081A-1
3	91	100.0	16	6	US-11-066-697-1536
4	37	40.7	16	3	US-09-775-805-44
5	37	40.7	16	3	US-09-775-805-67
6	37	40.7	16	3	US-09-775-805-75
7	37	40.7	16	3	US-09-775-805-89
8	37	40.7	16	3	US-09-862-849-1
9	37	40.7	16	3	US-09-894-018-199
10	37	40.7	16	3	US-09-894-594-66
11	37	40.7	16	4	US-10-103-395-230
12	37	40.7	16	4	US-10-114-716A-1
13	37	40.7	16	4	US-10-041-414-42
14	37	40.7	16	4	US-10-371-525-308
15	37	40.7	16	4	US-10-371-069-308
16	37	40.7	16	4	US-10-371-645-308
17	37	40.7	16	4	US-10-371-260-308
18	37	40.7	16	4	US-10-369-121-40
19	37	40.7	16	4	US-10-372-111-9
20	37	40.7	16	4	US-10-699-517-11
21	37	40.7	16	4	US-10-698-099-11
22	37	40.7	16	4	US-10-753-339-44
23	37	40.7	16	4	US-10-753-339-67
24	37	40.7	16	4	US-10-753-339-75
25	37	40.7	16	4	US-10-753-339-89
26	37	40.7	16	4	US-10-771-174A-10
27	37	40.7	16	5	US-10-889-999-51

28	37	40.7	16	5	US-10-890-070-51	Sequence 51, Appl
29	37	40.7	16	5	US-10-474-960A-199	Sequence 199, App
30	37	40.7	16	5	US-10-890-000-51	Sequence 51, Appl
31	37	40.7	16	5	US-10-823-463-51	Sequence 51, Appl
32	37	40.7	16	5	US-10-915-214-11	Sequence 11, Appl
33	37	40.7	16	5	US-10-822-968-51	Sequence 51, Appl
34	37	40.7	16	5	US-10-777-792-51	Sequence 51, Appl
35	37	40.7	16	5	US-10-890-071-51	Sequence 51, Appl
36	37	40.7	16	5	US-10-930-548-1	Sequence 1, Appl
37	37	40.7	16	5	US-10-890-024-51	Sequence 51, Appl
38	37	40.7	16	5	US-10-928-928-51	Sequence 51, Appl
39	37	40.7	16	6	US-11-058-757-51	Sequence 51, Appl
40	37	40.7	16	6	US-11-058-728-1	Sequence 1, Appl
41	34	37.4	16	3	US-09-911-838-225	Sequence 225, App
42	32	35.2	16	4	US-10-289-228-65	Sequence 65, Appl
43	32	35.2	16	4	US-10-373-592-119	Sequence 119, App
44	32	35.2	16	4	US-10-431-596-65	Sequence 65, Appl
45	32	35.2	16	6	US-11-102-403-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1

US-09-865-281A-1
; Sequence 1, Application US/09865281A
; Publication No. US20030103984A1
; GENERAL INFORMATION:
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: FUSION PROTEINS OF BIOLOGICALLY ACTIVE PEPTIDES AND ANTIBODIES
; FILE REFERENCE: 411.35629PC2
; CURRENT APPLICATION NUMBER: US/09/865,281A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/070,907
; PRIOR FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(16)
; OTHER INFORMATION: Synthesized peptide with sequence derived from position 1217-123
US-09-865-281A-1

Query Match 100.0%; Score 91; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNWEDPGKQLYNVEA 16
|||
Db 1 KNWEDPGKQLYNVEA 16

RESULT 2

US-10-795-081A-1
; Sequence 1, Application US/10795081A
; Publication No. US20050033033A1
; GENERAL INFORMATION:
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: TRANS-MEMBRANE-ANTIBODY INDUCED INHIBITION OF APOPTOSIS
; FILE REFERENCE: 411.35629AP3
; CURRENT APPLICATION NUMBER: US/10/795,081A
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: 60/451,980
; PRIOR FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 09/865,281
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/070,907
; PRIOR FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(16)
; OTHER INFORMATION: Synthesized peptide with sequence derived from position 1217-1232
US-10-795-081A-1

Query Match 100.0%; Score 91; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-07; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0;

Qy 1 KNRWDPGKQLYNVEA 16
|||||
Db 1 KNRWDPGKQLYNVEA 16

RESULT 3

US-11-066-697-1536
; Sequence 1536, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1536
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-1536

Query Match 100.0%; Score 91; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-07; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0;

Qy 1 KNRWDPGKQLYNVEA 16
|||||
Db 1 KNRWDPGKQLYNVEA 16

RESULT 4

US-09-775-805-44
; Sequence 44, Application US/09775805
; Publication No. US20010036461A1
; GENERAL INFORMATION:
; APPLICANT: DUKE UNIVERSITY
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-548
; CURRENT APPLICATION NUMBER: US/09/775,805
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497

; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Murine sp.
US-09-775-805-44

Query Match 40.7%; Score 37; DB 3; Length 16;
Best Local Similarity 45.5%; Pred. No. 76;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NRWDPGKOLY 12
|||
Db 5 NMWQEVGKAMY 15

RESULT 5

US-09-775-805-67
; Sequence 67, Application US/09775805
; Publication No. US20010036461A1
; GENERAL INFORMATION:
; APPLICANT: DUKE UNIVERSITY
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-548
; CURRENT APPLICATION NUMBER: US/09/775,805
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-805-67

Query Match 40.7%; Score 37; DB 3; Length 16;
Best Local Similarity 45.5%; Pred. No. 76;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NRWDPGKOLY 12
|||
Db 5 NMWQEVGKAMY 15

RESULT 6

US-09-775-805-75
; Sequence 75, Application US/09775805
; Publication No. US20010036461A1
; GENERAL INFORMATION:
; APPLICANT: DUKE UNIVERSITY
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-548
; CURRENT APPLICATION NUMBER: US/09/775,805
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV-1
; OTHER INFORMATION: Th-dominant/subdominant CTL epitopes in MVA.
US-09-775-805-75

Query Match 40.7%; Score 37; DB 3; Length 16;
Best Local Similarity 45.5%; Pred. No. 76;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
| | : : | | : |
Db 5 NMWQEVGKAMY 15

RESULT 7

US-09-775-805-89
; Sequence 89, Application US/09775805
; Publication No. US20010036461A1
; GENERAL INFORMATION:
; APPLICANT: DUKE UNIVERSITY
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-548
; CURRENT APPLICATION NUMBER: US/09/775,805
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV-1 Th-CTL
; OTHER INFORMATION: A2 p17 epitope (A2 Variants) in WVA
US-09-775-805-89

Query Match 40.7%; Score 37; DB 3; Length 16;
Best Local Similarity 45.5%; Pred. No. 76;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
| | : : | | : |
Db 5 NMWQEVGKAMY 15

RESULT 8

US-09-862-849-1
; Sequence 1, Application US/09862849
; Patent No. US20020013274A1
; GENERAL INFORMATION:
; APPLICANT: Sudhir Paul
; APPLICANT: Larry J. Smith
; APPLICANT: Gennady Gololobov
; TITLE OF INVENTION: Methods for Identifying Inducers and Inhibitors of Proteolytic
; FILE OF INVENTION: Antibodies, Compositions and Their Uses
; FILE REFERENCE: UNMC 63123 DIV
; CURRENT APPLICATION NUMBER: US/09/862,849
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/046,373
; PRIOR FILING DATE: 1998-03-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus-1
US-09-862-849-1

Query Match 40.7%; Score 37; DB 3; Length 16;
Best Local Similarity 45.5%; Pred. No. 76;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
| | : : | | : |
Db 5 NMWQEVGKAMY 15

RESULT 9

US-09-894-018-199
; Sequence 199, Application US/09894018

; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denisw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Transgenic mouse
US-09-894-018-199

Query Match 40.7%; Score 37; DB 3; Length 16;
Best Local Similarity 45.5%; Pred. No. 76;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
| | : : | | : |
Db 6 NMWQEVGKAMY 16

RESULT 10

US-09-894-594-66
; Sequence 66, Application US/09894594
; Publication No. US20030017497A1
; GENERAL INFORMATION:
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Weiner, David B.
; APPLICANT: Monzavi-Karbassi, Behjatolah
; TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens and DNA Molecules Enc
; TITLE OF INVENTION: Same
; FILE REFERENCE: UPN-3984
; CURRENT APPLICATION NUMBER: US/09/894,594
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 09/601,558
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: PCT/US99/02405
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 60/073,690
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: 60/214,517
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Novel Sequence
US-09-894-594-66

Query Match 40.7%; Score 37; DB 3; Length 16;
Best Local Similarity 45.5%; Pred. No. 76;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
| | : | : | : |
Db 5 NMWQEVGKAMY 15

RESULT 11

US-10-103-395-230
; Sequence 230, Application US/10103395
; Publication No. US20020160019A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
; TITLE OF INVENTION: RESTRICTED EPITOPES
; FILE REFERENCE: 39963-20016.01
; CURRENT APPLICATION NUMBER: US/10/103,395
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 09/009,953
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: PCT/US98/01373
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: US 60/036,713
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 60/037,432
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 230
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-395-230

Query Match 40.7%; Score 37; DB 4; Length 16;
Best Local Similarity 45.5%; Pred. No. 76;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
| | : | : | : |
Db 6 NMWQEVGKAMY 16

RESULT 12

US-10-114-716A-1
; Sequence 1, Application US/10114716A
; Publication No. US20030078203A1
; GENERAL INFORMATION:
; APPLICANT: Sudhir Paul
; APPLICANT: Yasuhiro Nishiyama
; TITLE OF INVENTION: Covalently Reactive Transition State
; TITLE OF INVENTION: Analogs and Methods of Use Thereof
; FILE REFERENCE: UTH001HB
; CURRENT APPLICATION NUMBER: US/10/114,716A
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 09/862,849
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/046,373
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 60/280,624
; PRIOR FILING DATE: 2001-03-31
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus-1
US-10-114-716A-1

Query Match 40.7%; Score 37; DB 4; Length 16;
Best Local Similarity 45.5%; Pred. No. 76;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
| | : | : | : |
Db 5 NMWQEVGKAMY 15

RESULT 13

US-10-041-414-42
; Sequence 42, Application US/10041414
; Publication No. US20030087225A1
; GENERAL INFORMATION:
; APPLICANT: SHIVER, JOHN W.
; APPLICANT: DAVIES, MARY ELLEN
; APPLICANT: FREED, DANIEL C.
; APPLICANT: LIU, MARGARET A.
; APPLICANT: PERRY, HELEN C.
; TITLE OF INVENTION: SYNTHETIC HIV ENV GENES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
; STREET: 126 E. LINCOLN AVE., - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/041,414
; FILING DATE: 08-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,368
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: HAND, J. MARK
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 19643
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-3905
; TELEFAX: 732-594-4720
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-041-414-42

Query Match 40.7%; Score 37; DB 4; Length 16;
Best Local Similarity 45.5%; Pred. No. 76;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
| | : | : | : |
Db 5 NMWQEVGKAMY 15

RESULT 14

US-10-371-525-308
; Sequence 308, Application US/10371525
; Publication No. US20030203869A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian

; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/10/371,525
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/311,784
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV1 ENV 566 (peptide F091.15)
US-10-371-525-308

Query Match 40.7%; Score 37; DB 4; Length 16;
Best Local Similarity 45.5%; Pred. No. 76;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
| | : | : |
Db 6 NMWQEVGKAMY 16

RESULT 15
US-10-371-069-308
; Sequence 308, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV1 ENV 566 (peptide F091.15)
US-10-371-069-308

Query Match 40.7%; Score 37; DB 4; Length 16;
Best Local Similarity 45.5%; Pred. No. 76;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
| | : | : |
Db 6 NMWQEVGKAMY 16

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Job time : 160 secs

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OM protein - protein search, using sw model

Run on: May 15, 2006, 16:51:11 ; Search time 27 Seconds
(without alignments)
27.822 Million cell updates/sec

Title: US-09-865-281A-1

Perfect score: 91

Sequence: 1 KNRWDPGKQLYNVEA 16

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Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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6: /SIDSS/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
7: /SIDSS/ptodata/1/pubpaa/US09_NEW_PUB.pep1.*
8: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
9: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB.pep1.*
10: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
11: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB.pep1.*
12: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	40.7	16	9 US-10-973-977-44	Sequence 44, Appl
2	37	40.7	16	9 US-10-973-977-67	Sequence 67, Appl
3	37	40.7	16	9 US-10-973-977-75	Sequence 75, Appl
4	37	40.7	16	9 US-10-973-977-89	Sequence 89, Appl
5	37	40.7	16	11 US-11-045-024-14479	Sequence 14479, A
6	37	40.7	16	11 US-11-115-425-88	Sequence 88, Appl
7	37	40.7	16	11 US-11-185-907-11	Sequence 11, Appl
8	32	35.2	16	11 US-11-056-950-226	Sequence 226, Appl
9	32	35.2	16	11 US-11-056-950-230	Sequence 230, Appl
10	32	35.2	16	11 US-11-056-950-234	Sequence 234, Appl
11	32	35.2	16	11 US-11-056-950-241	Sequence 241, Appl
12	30	33.0	16	11 US-11-056-950-54	Sequence 54, Appl
13	28	30.8	16	9 US-10-530-061-1652	Sequence 1652, Ap
14	27	29.7	16	11 US-11-056-950-185	Sequence 185, App
15	27	29.7	16	11 US-11-056-950-189	Sequence 189, App
16	27	29.7	16	11 US-11-056-950-193	Sequence 193, App
17	27	29.7	16	11 US-11-056-950-204	Sequence 204, App
18	26	28.6	16	11 US-11-056-950-208	Sequence 208, App
19	26	28.6	16	11 US-11-056-950-212	Sequence 212, App
20	26	28.6	16	11 US-11-056-950-216	Sequence 216, App
21	26	28.6	16	11 US-11-056-950-223	Sequence 223, App

22	26	28.6	16	11	US-11-223-699A-11	Sequence 11, Appl
23	26	28.6	16	11	US-11-121-566A-11	Sequence 11, Appl
24	26	28.6	16	11	US-11-152-974A-222	Sequence 222, App
25	26	28.6	16	11	US-11-153-143A-222	Sequence 222, App
26	25	27.5	16	11	US-11-056-950-30	Sequence 30, Appl
27	24	26.4	16	11	US-11-152-846-11	Sequence 11, Appl
28	24	26.4	16	11	US-11-207-078-103	Sequence 103, Appl
29	23.5	25.8	16	11	US-11-209-289-11	Sequence 11, Appl
30	23	25.3	16	9	US-10-461-904-2	Sequence 2, Appli
31	23	25.3	16	10	US-11-176-182-67	Sequence 67, Appl
32	23	25.3	16	11	US-11-152-846-2	Sequence 2, Appli
33	23	25.3	16	11	US-11-252-479-117	Sequence 117, App
34	22	24.2	16	9	US-10-834-397-238	Sequence 238, App
35	22	24.2	16	9	US-10-993-543-292	Sequence 292, App
36	22	24.2	16	11	US-11-106-415-15	Sequence 15, Appl
37	22	24.2	16	11	US-11-106-415-411	Sequence 411, Appl
38	22	24.2	16	11	US-11-233-256-15	Sequence 15, Appl
39	22	24.2	16	11	US-11-233-256-411	Sequence 411, Appl
40	21	23.1	16	9	US-10-201-525-40	Sequence 40, Appl
41	21	23.1	16	11	US-11-089-764-47	Sequence 47, Appl
42	21	23.1	16	11	US-11-054-515-2163	Sequence 2163, Ap
43	21	23.1	16	11	US-11-054-515-2838	Sequence 2838, Ap
44	21	23.1	16	11	US-11-054-515-3006	Sequence 3006, Ap
45	21	23.1	16	11	US-11-152-697-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-10-973-977-44
; Sequence 44, Application US/10973977
; Publication No. US2006008467A1
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: LIAO, HUA-XIN
; APPLICANT: LETVIN, NORMAN
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-942
; CURRENT APPLICATION NUMBER: US/10/973,977
; PRIOR FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/775,805
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Murine sp.
US-10-973-977-44

Query Match 40.7%; Score 37; DB 9; Length 16;
Best Local Similarity 45.5%; Pred. No. 6.4;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NNRWDPGKQLY 12
DB 5 NNRWDPGKQLY 15

RESULT 2
US-10-973-977-67
; Sequence 67, Application US/10973977
; Publication No. US2006008467A1
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: LIAO, HUA-XIN
; APPLICANT: LETVIN, NORMAN
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-942
; CURRENT APPLICATION NUMBER: US/10/973,977

; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/775,805
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-973-977-67

Query Match 40.7%; Score 37; DB 9; Length 16;
Best Local Similarity 45.5%; Pred. No. 6.4;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
| | : | : | : |
Db 5 NMWQEVGKAMY 15

RESULT 3
US-10-973-977-75
; Sequence 75, Application US/10973977
; Publication No. US2006008467A1
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: LIAO, HUA-XIN
; APPLICANT: LETVIN, NORMAN
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-942
; CURRENT APPLICATION NUMBER: US/10/973,977
; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/775,805
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV-1
; OTHER INFORMATION: Th-dominant/subdominant CTL epitopes in MVA.
US-10-973-977-75

Query Match 40.7%; Score 37; DB 9; Length 16;
Best Local Similarity 45.5%; Pred. No. 6.4;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
| | : | : | : |
Db 5 NMWQEVGKAMY 15

RESULT 4
US-10-973-977-89
; Sequence 89, Application US/10973977
; Publication No. US2006008467A1
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: LIAO, HUA-XIN
; APPLICANT: LETVIN, NORMAN
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-942
; CURRENT APPLICATION NUMBER: US/10/973,977
; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/775,805
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497

; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV-1 Th-CTL
; OTHER INFORMATION: A2 p17 epitope (A2 Variants) in MVA
US-10-973-977-89

Query Match 40.7%; Score 37; DB 9; Length 16;
Best Local Similarity 45.5%; Pred. No. 6.4;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
| | : | : | : |
Db 5 NMWQEVGKAMY 15

RESULT 5
US-11-045-024-14479
; Sequence 14479, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007 US/11/045,024
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14479
; LENGTH: 16
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY
US-11-045-024-14479

Query Match 40.7%; Score 37; DB 11; Length 16;
Best Local Similarity 45.5%; Pred. No. 6.4;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
| | : | : | : |
Db 6 NMWQEVGKAMY 16

RESULT 6
US-11-115-425-88
; Sequence 88, Application US/11115425
; Publication No. US2006001881A1
; GENERAL INFORMATION:
; APPLICANT: Shiver, John W
; Liu, Margaret A
; Perry, Helen C
; TITLE OF INVENTION: COORDINATE IN VIVO GENE EXPRESSION
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. Mark Hand
; STREET: 126 Lincoln Avenue, P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/115,425
; FILING DATE: 27-Apr-2005
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 19188YCB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (732) 594-3905
; TELEFAX: (732) 594-4720
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 88:
US-11-115-425-88

Query Match 40.7%; Score 37; DB 11; Length 16;
Best Local Similarity 45.5%; Pred. No. 6.4;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
|::||:
Db 5 NMWQEVGKAMY 15

RESULT 7
US-11-185-907-11
; Sequence 11, Application US/11185907
; Publication No. US2006005823A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceuticals, Inc.
; APPLICANT: Regents of the University of California
; APPLICANT: Schenk, Dale B.
; APPLICANT: Buttini, Manuel
; APPLICANT: Masliah, Eliezer
; APPLICANT: Chilcote, Tamie
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF SYNUCLEINOPATHIC DISEASE
; FILE REFERENCE: 015970-008950US
; CURRENT APPLICATION NUMBER: US/11/185,907
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: US 10/915,214
; PRIOR FILING DATE: 2004-08-09

; PRIOR APPLICATION NUMBER: US 10/699,517
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 10/698,099
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/423,012
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-185-907-11

Query Match 40.7%; Score 37; DB 11; Length 16;
Best Local Similarity 45.5%; Pred. No. 6.4;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
|::||:
Db 5 NMWQEVGKAMY 15

RESULT 8
US-11-056-950-226
; Sequence 226, Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
; APPLICANT: MICHELITSCH, Melissa D
; TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
; FILE REFERENCE: 2300-21026.20
; CURRENT APPLICATION NUMBER: US/11/056,950
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 10/917,646
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: 60/586,509
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/570,368
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/494,962
; PRIOR FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 226
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide
US-11-056-950-226

Query Match 35.2%; Score 32; DB 11; Length 16;
Best Local Similarity 35.7%; Pred. No. 44;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLYNVE 15
|::||:
Db 3 NQWNPSPKPTNMK 16

RESULT 9
US-11-056-950-230
; Sequence 230, Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
; APPLICANT: MICHELITSCH, Melissa D
; TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
; FILE REFERENCE: 2300-21026.20
; CURRENT APPLICATION NUMBER: US/11/056,950
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 10/917,646
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: 60/586,509

; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/570,368
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/494,962
; PRIOR FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 230
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide
; US-11-056-950-230

Query Match 35.2%; Score 32; DB 11; Length 16;
Best Local Similarity 35.7%; Pred. No. 44;
Matches 5; Conservative 3; Mismatches 6; Indels 6; Gaps 0;

QY 2 NRWEDPGKQLYNVE 15
|:|:|:|:|:|:
Db 2 NQWNKPSKPKTNMK 15

RESULT 10

US-11-056-950-234
; Sequence 234, Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
; APPLICANT: MICHELITSCH, Melissa D
; TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
; FILE REFERENCE: 2300-21026.20
; CURRENT APPLICATION NUMBER: US/11/056,950
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 10/917,646
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: 60/586,509
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/570,368
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/494,962
; PRIOR FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 234
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide
; US-11-056-950-234

Query Match 35.2%; Score 32; DB 11; Length 16;
Best Local Similarity 35.7%; Pred. No. 44;
Matches 5; Conservative 3; Mismatches 6; Indels 6; Gaps 0;

QY 2 NRWEDPGKQLYNVE 15
|:|:|:|:|:|:
Db 1 NQWNKPSKPKTNMK 14

RESULT 11

US-11-056-950-241
; Sequence 241, Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
; APPLICANT: MICHELITSCH, Melissa D
; TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
; FILE REFERENCE: 2300-21026.20
; CURRENT APPLICATION NUMBER: US/11/056,950
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 10/917,646
; PRIOR FILING DATE: 2004-08-13

; PRIOR APPLICATION NUMBER: 60/586,509
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/570,368
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/494,962
; PRIOR FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 241
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide
; US-11-056-950-241

Query Match 35.2%; Score 32; DB 11; Length 16;
Best Local Similarity 35.7%; Pred. No. 44;
Matches 5; Conservative 3; Mismatches 6; Indels 6; Gaps 0;

QY 2 NRWEDPGKQLYNVE 15
|:|:|:|:|:|:
Db 1 NQWNKPSKPKTNMK 14

RESULT 12

US-11-056-950-54
; Sequence 54, Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
; APPLICANT: MICHELITSCH, Melissa D
; TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
; FILE REFERENCE: 2300-21026.20
; CURRENT APPLICATION NUMBER: US/11/056,950
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 10/917,646
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: 60/586,509
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/570,368
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/494,962
; PRIOR FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 54
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide
; US-11-056-950-54

Query Match 33.0%; Score 30; DB 11; Length 16;
Best Local Similarity 41.7%; Pred. No. 95;
Matches 5; Conservative 1; Mismatches 6; Indels 6; Gaps 0;

QY 2 NRWEDPGKQLYN 13
|:|:|:|:|:|:
Db 5 NQWNKPSKPKTN 16

RESULT 13

US-10-530-061-1652
; Sequence 1652, Application US/10530061
; Publication No. US20060079453A1
; GENERAL INFORMATION:
; APPLICANT: SIDNEY, JOHN
; APPLICANT: SOUTHWOOD, SCOTT
; APPLICANT: SETTE, ALESSANDRO
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; FILE REFERENCE: 2060.033US02/EKS/M-M
; CURRENT APPLICATION NUMBER: US/10/530,061


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: CURRENT FILING DATE: 2005-04-04
: PRIOR APPLICATION NUMBER: PCT/US03/31308
: PRIOR FILING DATE: 2003-10-03
: PRIOR APPLICATION NUMBER: 60/416,207
: PRIOR FILING DATE: 2003-10-03
: PRIOR APPLICATION NUMBER: 60/417,269
: PRIOR FILING DATE: 2003-10-08
: NUMBER OF SEQ ID NOS: 2503
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 1652.
: LENGTH: 16
: TYPE: PRT
: ORGANISM: Human immunodeficiency virus
US-10-530-061-1652

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Query Match      30.8%; Score 28; DB 9; Length 16;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels

Qy      4 WEDPGKQ 10
      | | | |
Db      4 WNHFGSO 10

```

Query Match	29.7%;	Score 27;	DB 11;	Length 16;
Best Local Similarity	28.6%;	Pred. No. 3e+02;		
Matches	4;	Conservative	4;	Mismatches 6; Indels
QY	2	NRWEDFGQLYNVE	15	
	:	:	:	:
Db	3	SQWNKPSKPKTNMK	16	

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; PRIOR APPLICATION NUMBER: 60/586,586
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/570,368
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/494,962
; PRIOR FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 189
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide
US-11-056-950-189

```

Query Match	29.7%	Score 27;	DB 11;	Length 16;
Best Local Similarity	28.6%	Pred. No.	3e-02;	
Matches	4;	Conservative	4;	Mismatches 6; Indels 0; Gaps 0;
Qy	2	NRWEDFGKQLYNYE	15	
Dd	2	SOWNKFSKPKNMK	15	
	:		:	:
	:		:	:
	:		:	:

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OM protein - protein search, using sw model

Run on: May 15, 2006, 16:35:21 ; Search time 38 seconds
(without alignments)
40.512 Million cell updates/sec

Title: US-09-865-281A-1
Perfect score: 91
Sequence: 1 KNREDPGKQLYNVEA 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 250

Minimum DB seq length: 16
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	30.8	16	G24304	ribosomal protein
2	23	25.3	16	A31963	pyruvate dehydrog
3	22	24.2	16	PT0282	Ig heavy chain CDR
4	20	22.0	16	MTDFBS	melanotropin beta
5	19	20.9	16	D49021	Ig heavy chain J7
6	19	20.9	16	PL0137	protein kinase, 80
7	19	20.9	16	B44896	heat shock protein
8	18	19.8	16	B47014	orf2 3' of chrR -
9	18	19.8	16	PH0773	T-cell receptor be
10	18	19.8	16	A48630	bothrojaracin - ja
11	18	19.8	16	S13898	alkaline phosphata
12	17	18.7	16	B60560	formyltetrahydrofo
13	17	18.7	16	PH0137	T-cell receptor be
14	17	18.7	16	A49255	T-cell receptor be
15	17	18.7	16	B28587	T-cell receptor be
16	17	18.7	16	F53284	T-cell receptor be
17	17	18.7	16	PH1604	Ig H chain V-D-J r
18	17	18.7	16	PC1299	subtilisin (EC 3.4
19	17	18.7	16	A59155	multicystatin - to
20	17	18.7	16	S38292	30K allergen - rye
21	16	17.6	16	C45143	protein-tyrosine-p
22	16	17.6	16	H41299	T-cell receptor al
23	16	17.6	16	E53284	T-cell receptor be
24	16	17.6	16	D49037	TcR delta chain V-
25	16	17.6	16	S42237	hypothetical prote
26	16	17.6	16	A20190	hypodermin B - ear
27	16	17.6	16	S54271	GATA-2 protein - A
28	16	17.6	16	I79565	hypothetical TCL3/
29	15	16.5	16	A29541	little gastrin - C

30	15	16.5	16	2	PH0759	T-cell receptor be
31	15	16.5	16	2	A45454	ankyrin-binding gl
32	15	16.5	16	2	S11760	flgI protein - Cau
33	15	16.5	16	2	I51879	cystathionine beta
34	15	16.5	16	2	C37290	homeotic protein G
35	14.5	15.9	16	2	PH0791	T-cell receptor al
36	14	15.4	16	2	A59042	alpha-conotoxin Bp
37	14	15.4	16	2	S03532	Ig heavy chain J r
38	14	15.4	16	2	A28144	ribosomal protein
39	14	15.4	16	2	S34444	blaz protein - Sta
40	14	15.4	16	2	S28213	glutathione transf
41	14	15.4	16	2	PT0237	Ig heavy chain CDR
42	14	15.4	16	2	G24687	T-cell receptor be
43	14	15.4	16	2	E58503	superoxide dismuta
44	14	15.4	16	2	B44820	7K protein - Esche
45	14	15.4	16	2	A49226	major outer membra

ALIGNMENTS

RESULT 1

G24304
ribosomal protein H [validated] - Haloarcula marismortui (fragment)
C:Species: Haloarcula marismortui
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 21-Jul-2000
C:Accession: G24304
R:Shoham, M.; Dijk, J.; Reinhardt, R.; Wittmann-Liebold, B.
FEBS Lett. 204, 323-330, 1986
A:Title: Purification and characterization of ribosomal proteins from the 30 S subunit
A:Reference number: A24304
A:Accession: G24304
A:Molecule type: protein
A:Residues: 1-16 <SHO>
A:Cross-references: UNIPARC:UPI000017AEA2
C:Keywords: protein biosynthesis; ribosome

Query Match 30.8%; Score 28; DB 2; Length 16;
Best Local Similarity 55.6%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 PGKQLYNVE 15
||| : |||
DB 1 PGNKYND 9

RESULT 2

A31963
pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain type I - pig roundworm (fra
C:Species: Ascaris suum (pig roundworm)
C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C:Accession: A31963
R:Thissen, J.; Komuniecki, R.
J. Biol. Chem. 263, 19092-19097, 1988
A:Title: Phosphorylation and inactivation of the pyruvate dehydrogenase from the anaerob
A:Reference number: A31963; MUID:89066711; PMID:3198613
A:Accession: A31963
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <THI>
A:Cross-references: UNIPROT:P26267; UNIPARC:UPI000017B69C
C:Keywords: mitochondrion; oxidoreductase; phosphoprotein

Query Match 25.3%; Score 23; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 DPGKQLY 12
||| : |||
DB 9 DPGTSSY 15

RESULT 3

PT0282
 IG heavy chain CDR3 region (clone 4-94A) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0282
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
 A;Reference number: PT0222; MUID:91108337; PMID:1899102
 A;Accession: PT0282
 A;Molecule type: DNA
 A;Residues: 1-16 <YAM>
 A;Cross-references: UNIPARC:UPI000017C1DA
 A;Experimental source: B lymphocyte
 C;Keywords: heterotetramer; immunoglobulin

Query Match 24.2%; Score 22; DB 2; Length 16;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 WEDPGKQ 10
 |||||
 Db 8 WFDWVGQ 14

RESULT 4
 MTDPBS
 melanotropin beta - spiny dogfish
 C:Species: Squalus acanthias (spiny dogfish)
 C>Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004
 C:Accession: A01471
 R;Bennett, H.P.J.; Lowry, P.J.; McMartin, C.; Scott, A.P.
 Biochem. J. 141, 439-444, 1974
 A>Title: Structural studies of alpha-melanocyte-stimulating hormone and a novel beta-mel
 A;Reference number: A90277; MUID:75127390; PMID:4375978
 A;Accession: A01471
 A;Molecule type: protein
 A;Residues: 1-16 <BEN>
 A;Cross-references: UNIPROT:P01207; UNIPARC:UPI000012F1C2
 C;Superfamily: corticotropin-lipotropin
 C;Keywords: hormone

Query Match 22.0%; Score 20; DB 1; Length 16;
 Best Local Similarity 60.0%; Pred. No. 5.8e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 RWEDP 7
 |||||
 Db 11 RWSVP 15

RESULT 5
 D49021
 IG heavy chain J7 region - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
 C:Accession: D49021
 R;Haire, R.N.; Anemiya, C.T.; Suzuki, D.; Litman, G.W.
 J. Exp. Med. 171, 1721-1737, 1990
 A>Title: Eleven distinct V-H gene families and additional patterns of sequence variation
 A;Reference number: A47624; MUID:90237760; PMID:2110243
 A;Accession: D49021
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-16 <HAI>
 A;Cross-references: UNIPARC:UPI000017692C
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin

Query Match 20.9%; Score 19; DB 2; Length 16;
 Best Local Similarity 75.0%; Pred. No. 8.4e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RWED 6
 |||||
 Db 1 RWFD 4

RESULT 6
 PL0137
 protein kinase, 80K - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 18-Jun-1993
 C:Accession: PL0137
 R;Dechert, U.; Weber, M.; Weber-Schaeuffelen, M.; Wollny, E.
 J. Neurochem. 53, 1268-1275, 1989
 A>Title: Isolation and partial characterization of an 80,000-dalton protein kinase from
 A;Reference number: PL0137; MUID:89361455; PMID:2769266
 A;Accession: PL0137
 A;Molecule type: protein
 A;Residues: 1-16 <DEC>
 A;Cross-references: UNIPARC:UPI0000177D3E
 C;Comment: This protein has a novel serine/threonine-specific protein kinase activity.

Query Match 20.9%; Score 19; DB 2; Length 16;
 Best Local Similarity 80.0%; Pred. No. 8.4e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 EDPGK 9
 |||||
 Db 12 EDLGG 16

RESULT 7
 B44896
 heat shock protein 18 - Streptomyces albus (fragment)
 C:Species: Streptomyces albus
 C>Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: B44896
 R;Guglielmi, G.; Mazodier, P.; Thompson, C.J.; Davies, J.
 J. Bacteriol. 173, 7374-7381, 1991
 A>Title: A survey of the heat shock response in four Streptomyces species reveals two g
 A;Reference number: A44896; MUID:92041638; PMID:1682303
 A;Accession: B44896
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-16 <GUG>
 A;Cross-references: UNIPROT:Q9R663; UNIPARC:UPI000017AD8C
 A;Note: sequence extracted from NCBI backbone (NCBIP:65107)

Query Match 20.9%; Score 19; DB 2; Length 16;
 Best Local Similarity 50.0%; Pred. No. 8.4e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 WEDPGKQ 11
 :||: |||
 Db 6 YENLGAQL 13

RESULT 8
 B47014
 orf2 3' of chuR - Bacteroides thetaiotaomicron (fragment)
 C:Species: Bacteroides thetaiotaomicron
 C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
 C:Accession: B47014
 R;Cheng, Q.; Hwa, V.; Salyers, A.A.
 J. Bacteriol. 174, 7185-7193, 1992
 A>Title: A locus that contributes to colonization of the intestinal tract by Bacteroid
 A;Reference number: A47014; MUID:93054330; PMID:1429442
 A;Accession: B47014
 A;Status: preliminary
 A;Molecule type: nucleic acid
 A;Residues: 1-16 <CHE>
 A;Cross-references: UNIPARC:UPI000017AB49
 A;Note: sequence extracted from NCBI backbone (NCBIN:118015, NCBIP:118017)

```
Query Match      19.8%; Score 18; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 KOLYN 13
DB 12 QOLYN 16

RESULT 9
PH0773
T-cell receptor beta chain (C7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0773
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0773
A:Molecule type: mRNA
A:Residues: 1-16 <AS>
A:Cross-references: UNIPARC:UPI0000115FC0; EMBL:X60868; NID:g50247; PIDN:CAA43257.1; PID
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match      19.8%; Score 18; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 5; Conservative 1; Mismatches 0; Indels 4; Gaps 1;

QY 7 PGK----QLY 12
DB 5 PQGLTGQLY 14

RESULT 10
A48630
bothrojaracin - jararaca (fragment)
N:Alternate names: thrombin inhibitor
C:Species: Bothrops jararaca (jararaca)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A48630
R:Zingali, R.B.; Jandrot-Perrus, M.; Guillin, M.C.; Bon, C.
Biochemistry 32, 10794-10802, 1993
A:Title: Bothrojaracin, a new thrombin inhibitor isolated from Bothrops jararaca venom:
A:Reference number: A48630; MUID:94002075; PMID:8399228
A:Accession: A48630
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-16 <ZIN>
A:Cross-references: UNIPROT:Q9PR24; UNIPARC:UPI000000FD244
A:Experimental source: venom
A:Note: sequence extracted from NCBI backbone (NCBIP:138787)

Query Match      19.8%; Score 18; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 1.2e+04;
Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 WEDPGKQLY 12
DB 6 WSPYGGQCY 14

RESULT 11
SI3898
alkaline phosphatase (EC 3.1.3.1) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: SI3898
R:Fujimori-Arai, Y.; Koyama, I.; Hirano, K.; Sakagishi, Y.; Komoda, T.
Arch. Biochem. Biophys. 284, 320-325, 1991
A:Title: Purification and partial characterization of intestinal-like alkaline phosphata
```

```
A:Reference number: SI3898; MUID:91112827; PMID:1989515
A:Accession: SI3898
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-16 <FUJ>
A:Cross-references: UNIPROT:Q7M2K8; UNIPARC:UPI000017CSB6
C:Keywords: phosphoric monoester hydrolase

Query Match      19.8%; Score 18; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EDP 7
DB 7 EDP 9

RESULT 12
B60560
formyltetrahydrofolate dehydrogenase (EC 1.5.1.6) / aldehyde dehydrogenase (NADP) (EC 1
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 31-Dec-2004
C:Accession: B60560
R:Johlin, F.C.; Swain, E.; Smith, C.; Tephly, T.R.
Mol. Pharmacol. 35, 745-750, 1989
A:Title: Studies on the mechanism of methanol poisoning: purification and comparison of
A:Reference number: A60560; MUID:89281497; PMID:2733692
A:Accession: B60560
A:Molecule type: protein
A:Residues: 1-16 <JOH>
A:Cross-references: UNIPROT:Q8TBP8; UNIPARC:UPI000017CE07
C:Superfamily: 10-formyltetrahydrofolate dehydrogenase
C:Keywords: multifunctional enzyme; NADP; oxidoreductase

Query Match      18.7%; Score 17; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 GKOLY 12
DB 12 GOEYV 16

RESULT 13
PH0137
T-cell receptor beta chain V-D-J region MS20 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 30-May-1997
C:Accession: PH0137
R:Martin, R.; Howell, M.D.; Jaraquemada, D.; Flerlage, M.; Richert, J.; Brostoff, S.; L
J. Exp. Med. 173, 19-24, 1991
A:Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the conte
A:Reference number: PH0135; MUID:91086843; PMID:1702137
A:Accession: PH0137
A:Molecule type: mRNA
A:Residues: 1-16 <MAR>
A:Cross-references: UNIPARC:UPI0000017C3AF
C:Keywords: T-cell receptor

Query Match      18.7%; Score 17; DB 2; Length 16;
Best Local Similarity 27.3%; Pred. No. 1.8e+04;
Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 NRWEDPGKQLY 12
DB 6 SRKDSPPSPLH 16

RESULT 14
A49255
T-cell receptor beta chain V-D-J-C region (V beta 7, J beta 1.6) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
```

C;Accession: A49255
R;Rosenberg, W.M.; Moss, P.A.; Bell, J.I.
Eur. J. Immunol. 22, 541-549, 1992
A;Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using
A;Reference number: A49039; MUID:92164737; PMID:1311263
A;Accession: A49255
A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid
A;Residues: 1-16 <ROS>
A;Cross-references: UNIPARC:UPI000017C3B9
A;Note: sequence extracted from NCBI backbone (NCBIP:90722)
C;Keywords: T-cell receptor

Query Match 18.7%; Score 17; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 1.8e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 PGKQ 10
Db |||
6 PGTQ 9

RESULT 15

B28587
T-cell receptor beta-2 chain J-B2.3 segment - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
C;Accession: B28587
R;Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
A;Title: Organization and sequences of the diversity, joining, and constant region genes
A;Reference number: A94081; MUID:86094276; PMID:3866244
A;Accession: B28587
A;Molecule type: DNA
A;Residues: 1-16 <TOY>
A;Cross-references: UNIPARC:UPI000002FD06; GB:M14159; NID:g338852; PIDN:AAA60677.1; PID:
C;Keywords: T-cell receptor

Query Match 18.7%; Score 17; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.8e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 PGKQL 11
Db |||:
9 PGTRL 13

Search completed: May 15, 2006, 16:39:41
Job time : 39 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 16:34:51 ; Search time 224 Seconds
(without alignments)
50.395 Million cell updates/sec

Title: US-09-865-281A-1

Perfect score: 91

Sequence: 1 KNRWDPGKQLYNVEA 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 1144

Minimum DB seq length: 16

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	27.5	16	2 FIBLY3 SOLTU	Q7dly3 solanum tub
2	22	24.2	16	1 FIBA RABIT	P14461 oryctolagus
3	22	24.2	16	2 Q9TWC0 ACACA	Q9tvc0 acanthamoeb
4	22	24.2	16	2 Q4TSR1 SSPHN	Q4tsr1 erythrobact
5	22	24.2	16	2 Q691Z1 ANOSA	Q691z1 anolis sagr
6	21	23.1	16	2 Q21922 9CAUD	Q21922 streptococc
7	20	22.0	16	1 MLB SQUAC	P01207 squalus aca
8	20	22.0	16	2 Q9UR86 CANPA	Q9ur86 candida par
9	20	22.0	16	2 Q9NY32 HUMAN	Q9ny32 homo sapien
10	19.5	21.4	16	2 Q7W227 PSEAE	Q7w227 pseudomonas
11	19	20.9	16	2 Q9UCW4 HUMAN	Q9ucw4 homo sapien
12	19	20.9	16	2 Q5C7F3 SCHUA	Q5c7f3 schistosoma
13	19	20.9	16	2 Q7SM54 9DELA	Q7sm54 human t-lym
14	18	19.8	16	2 Q53SB3 HUMAN	Q53sb3 homo sapien
15	18	19.8	16	2 Q7M2K8 RABIT	Q7m2k8 oryctolagus
16	18	19.8	16	2 Q9T2Q6 SOLTU	Q9t2q6 solanum tub
17	18	19.8	16	2 Q4QIV4 SACOF	Q4qiv4 saccharum o
18	18	19.8	16	2 Q5MG28 COETO	Q5mg28 coeligena t
19	18	19.8	16	2 Q9PRZ4 BOTJA	Q9prz4 bothriops ja
20	17.5	19.2	16	1 AFP2S MALPA	P83142 malva parvi
21	17	18.7	16	1 SAL3 ONCMY	P82240 oncorhynchu
22	17	18.7	16	2 Q7S047 NEUCR	Q7s047 neurospora
23	17	18.7	16	2 Q8MM83 9NEOP	Q8mm83 heliconius
24	17	18.7	16	2 Q8MM84 9NEOP	Q8mm84 heliconius
25	17	18.7	16	2 Q8MM85 9NEOP	Q8mm85 heliconius
26	17	18.7	16	2 Q8MUN3 9NEOP	Q8mun3 heliconius
27	17	18.7	16	2 Q8MUN5 9NEOP	Q8mun5 heliconius
28	17	18.7	16	2 Q4X8S1 PLACH	Q4x8s1 plasmodium
29	17	18.7	16	2 Q95W79 HORSE	Q95w79 equus cabal
30	17	18.7	16	2 Q9TR88 BOVIN	Q9tr88 bos taurus
31	17	18.7	16	2 Q7M1V9 LYCES	Q7m1v9 lycopersico

RESULT 1

ID	Q7DLY3 SOLTU	PRELIMINARY;	PRT;	16 AA.
AC	Q7DLY3 SOLTU			
DT	05-JUL-2004 (Tremblrel. 27, Created)			
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)			
DE	Beta-fructofuranosidase (Invertase) (BC 3.2.1.26) (Fragment).			
OS	Solanum tuberosum (Potato).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	lamids; Solanales; Solanaceae; Solanum.			
OX	NCBI_TaxID=4113;			
RP	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=96279736; PubMed=8710506; DOI=10.1093/nar/24.12.2347;			
RA	Bournay A.S., Hedley P.E., Maddison A., Waugh R., Machray G.C.;			
RT	"Exon skipping induced by cold stress in a potato invertase gene transcript.";			
RL	Nucleic Acids Res. 24:2347-2351(1996).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Maddison A.L.;			
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; X95820; CAA65086.1; -; Genomic DNA.			
DR	GO; GO:0004564; F.beta-fructofuranosidase activity; IEA.			
DR	GO; GO:0016798; F.hydrolase activity, acting on glycosyl bonds; IEA.			
DR	GO; GO:0005975; P.carbohydrate metabolism; IEA.			
KW	Glycosidase; Hydrolase.			
FT	NON_TER 1			
FT	NON_TER 16			
SQ	SEQUENCE 16 AA; 1894 MW; 003053E73810C336 CRC64;			

Query Match 27.5%; Score 25; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 4.6e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 KNRWDPGKQLY 12

DB 2 KRWINDPNAPY 13

RESULT 2

ID	FIBA RABIT	STANDARD;	PRT;	16 AA.
AC	P14461			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DE	Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).			
GN	Name=FGA;			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;			

```
OC Oryctolegus.
OX NCBI_TaxID=9986;
RN [1]
RP PROTEIN SEQUENCE.
RT Blomback B., Blomback M., Grondahl N.J.;
RL "Studies on fibrinopeptides from mammals.";
Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: Heterohexamer; disulfide linked. Contains 2 sets of 3
CC nonidentical chains (alpha, beta and gamma). The 2 heterotrimers
CC are in head to head conformation with the N-termini in a small
CC central domain (By similarity).
CC -!- DOMAIN: A long coiled coil structure formed by 3 polypeptide
CC chains connects the central nodule to the C-terminal domains
CC (distal nodules). The long C-terminal ends of the alpha chains
CC fold back, contributing a fourth strand to the coiled coil
CC structure.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Blood coagulation; Coiled coil; Direct protein sequencing; Plasma.
KW PEPTIDE 1 16 Fibrinopeptide A.
FT NON_TER 16 16
FT SEQUENCE 16 AA; 1651 MW; DFB623279EA55EB6 CRC64;

Query Match 24.2%; Score 22; DB 1; Length 16;
Best Local Similarity 42.9%; Pred. No. 1.5e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 6 DPGKQLY 12
Db 2 DPGESTF 8

RESULT 3
O9TWC0 ACACA PRELIMINARY; PRT; 16 AA.
AC O9TWC0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Actin (Fragment).
OS Acanthamoeba castellanii (Amoeba).
OC Eukaryota; Acanthamoebidae; Acanthamoeba.
OX NCBI_TaxID=5755;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95014701; PubMed=7929556; DOI=10.1083/jcb.127.1.107;
RA Machesky L.M., Atkinson S.J., Ampe C., Vandekerckhove J.,
RA Pollard T.D.;
RT "Purification of a cortical complex containing two unconventional
RT actins from Acanthamoeba by affinity chromatography on profilin-
RT agarose.";
RL J. Cell Biol. 127:107-115(1994).
SQ SEQUENCE 16 AA; 2115 MW; A64E248880BA06C4 CRC64;

Query Match 24.2%; Score 22; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 WED 6
Db 2 WED 4
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RESULT 4
O4TSR1 9SPHN PRELIMINARY; PRT; 16 AA.
AC O4TSR1;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=ELI0115;
OS Erythrobacter litoralis HTCC2594.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Erythrobacter.
OX NCBI_TaxID=314225;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HTCC2594;
RA Giovannoni S.J., Cho J.-C., Ferriera S., Johnson J., Kravitz S.,
RA Halpern A., Remington K., Beeson K., Tran B., Rogers Y.-H.,
RA Friedman R., Venter J.C.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAGG01000001; EAL76309.1; -; Genomic_DNA.
DR Hypothetical protein.
KW SEQUENCE 16 AA; 1864 MW; 4D15F5FE0BA28A1E CRC64;

Query Match 24.2%; Score 22; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 RWED 6
Db 2 RWED 5

RESULT 5
Q691Z1 ANOSA PRELIMINARY; PRT; 16 AA.
ID Q691Z1 ANOSA PRELIMINARY; PRT; 16 AA.
AC Q691Z1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
OS Anolis sagrei (Brown anole).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=38937;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15356629; DOI=10.1038/nature02807;
RA Kolbe J.J., Glor R.E., Rodriguez Schettino L., Chamizo Lara A.,
RA Larson A., Losos J.B.;
RT "Genetic variation increases during biological invasion by a Cuban
RT lizard.";
RL Nature 431:177-181(2004).
DR EMBL; AY655188; AAT78035.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000883; COX1.
DR PANTHER; PTHR10422; COX1; 1.
KW Mitochondrion.
FT NON_TER 16 16
FT SEQUENCE 16 AA; 1953 MW; B0C8C72FF7493A35 CRC64;

Query Match 24.2%; Score 22; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2 NRW 4
   |||
Db 4 NRW 6

RESULT 6
O21922_9CAUD PRELIMINARY; PRT; 16 AA.
AC O21922_021923;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Integrase (Fragment).
GN Name=Int;
OS Streptococcus thermophilus bacteriophage Sfi21.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=64186;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98008989; PubMed=9344917; DOI=10.1006/viro.1997.8769;
RA Bruttin A., Foley S., Brussow H.;
RT "The site-specific integration system of the temperate Streptococcus
thermophilus bacteriophage phiSfi21.";
RL Virology 237:148-158(1997).
DR EMBL; AF013584; AAC48909.1; -; Genomic DNA.
DR EMBL; AF013587; AAC48910.1; -; Genomic DNA.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1856 MW; 8FA82D3270B9A959 CRC64;

Query Match 23.1%; Score 21; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 2.2e+04;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KNRWEDPGK 9
   |||
Db 1 KQWTECGR 9

RESULT 7
MLB_SQUAC STANDARD; PRT; 16 AA.
AC P01207;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Melanotropin beta.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Hypnosqualea; Squaliformes; Squaloidei;
OC Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=75127390; PubMed=4375978;
RA Bennett H.P.J., Lowry P.J., McMartin C., Scott A.P.;
RT "Structural studies of alpha-melanocyte-stimulating hormone and a
novel beta-melanocyte-stimulating hormone from the neurointermediate
lobe of the pituitary of the dogfish Squalus acanthias.";
RL Biochem. J. 141:439-444(1974).
CC -!- SIMILARITY: Belongs to the POMC family.
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CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR PIR; A01471; MTDPRS.
KW Direct protein sequencing; Hormone.
SQ SEQUENCE 16 AA; 1939 MW; 99AF43C8A640A0E CRC64;

Query Match 22.0%; Score 20; DB 1; Length 16;

Best Local Similarity 60.0%; Pred. No. 3.3e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 RWEDP 7
   |||
Db 11 RWSVP 15

RESULT 8
OSUR86_CANPA PRELIMINARY; PRT; 16 AA.
ID OSUR86_CANPA PRELIMINARY;
AC Q9UR86;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE Class I cytochrome C isoform A (Fragment).
OS Candida parapsilosis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5480;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93305688; PubMed=8391313; DOI=10.1016/0005-2728(93)90135-3;
RA Camougrand N., Velours J., Denis M., Guerin M.;
RT "Isolation, characterization and function of the two cytochromes c of
the yeast Candida parapsilosis.";
RL Biochim. Biophys. Acta 1143:135-141(1993).
SQ SEQUENCE 16 AA; 1646 MW; 762FF64F875F237B CRC64;

Query Match 22.0%; Score 20; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 3.3e+04;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 EDPGKQL 11
   |||||
Db 9 EPGASL 15

RESULT 9
OSNY32_HUMAN PRELIMINARY; PRT; 16 AA.
ID OSNY32_HUMAN PRELIMINARY;
AC Q9NY32;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Homo sapiens IL11 interleukin-1 like protein 1, exons 1-6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20545212; PubMed=11093146;
RA DOI=10.1002/1521-4141(200011)30:11<3299::AID-IMMUJ299>3.0.CO;2-S;
RA Barton J.L., Herbst R., Bosio D., Higgins L., Nicklin M.J.H.;
RT "A tissue specific IL-1 receptor antagonist homolog from the IL-1
cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.";
RL Eur. J. Immunol. 30:3299-3308(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Nicklin M.J.H.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ271338; CAB67703.1; -; Genomic DNA.
SQ SEQUENCE 16 AA; 1804 MW; 47FF677F8B6D87E CRC64;

Query Match 22.0%; Score 20; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 3.3e+04;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KNRWEDPGK 10
   |||
Db 7 RGRKEGEGE 16
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RESULT 10
Q7WZ27_PSEAE
ID Q7WZ27_PSEAE PRELIMINARY; PRT; 16 AA.
AC Q7WZ27
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative radical activating enzyme (Fragment).
GN Name=PA0975;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PA14;
RX PubMed=14983043; DOI=10.1073/pnas.0304622101;
RA He J., Baldini R.L., Dezziel E., Saucier M., Zhang Q., Liberati N.T.,
RA Lee D., Urbach J., Goodman H.M., Rahme L.G.;
RT "The broad host range pathogen Pseudomonas aeruginosa strain PA14
RT carries two pathogenicity islands harboring plant and animal virulence
RT genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2530-2535 (2004).
DR EMBL; AY273870; AAP82945.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 16 AA; 1941 MW; 1DD9B5D22AF6B7C CRC64;

Query Match 21.48; Score 19.5; DB 2; Length 16;
Best Local Similarity 66.74; Pred. No. 4.1e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 4 WED-PG 8
DB 10 WNDEPG 15

RESULT 11
Q9UCW4_HUMAN
ID Q9UCW4_HUMAN PRELIMINARY; PRT; 16 AA.
AC Q9UCW4
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Dystrophin isoform (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96081207; PubMed=8541829;
RA Austin R.C., Howard P.L., D'Souza V.N., Klamut H.J., Ray P.N.;
RT "Cloning and characterization of alternatively spliced isoforms of
RT Dp71.";
RL Hum. Mol. Genet. 4:1475-1483 (1995).
SQ SEQUENCE 16 AA; 1833 MW; E0CFAP3B5C85BBF CRC64;

Query Match 20.98; Score 19; DB 2; Length 16;
Best Local Similarity 60.04; Pred. No. 5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 PGKOL 11
DB 7 PGKPM 11

RESULT 12
Q5C7F3_SCHJA
ID Q5C7F3_SCHJA PRELIMINARY; PRT; 16 AA.
AC Q5C7F3;

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DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY808532; AAX24421.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 16 AA; 1945 MW; 7369A9EAB699AC65 CRC64;

Query Match 20.9%; Score 19; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 5e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 LYNV 14
DB 1 MYNV 4

RESULT 13
Q7SM54_9DELA
ID Q7SM54_9DELA PRELIMINARY; PRT; 16 AA.
AC Q7SM54;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tax protein (Fragment).
OS Human T-lymphotropic virus 1.
OC Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gonzalez Perez M.P., Garcia Saiz A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF529962; AAP87693.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 16 AA; 1782 MW; 9CDDDFE4146EA2F CRC64;

Query Match 20.9%; Score 19; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 5e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 EDPGKQ 10
DB 4 EPPGEX 9

RESULT 14
Q53SB3_HUMAN
ID Q53SB3_HUMAN PRELIMINARY; PRT; 16 AA.
AC Q53SB3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein SLC4A10 (Fragment).
GN Name=SLC4A10; (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Belter E., Kozlowski A., Dixon R.;
RT "The sequence of Homo sapiens BAC clone RP11-220I15.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]

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RP NUCLEOTIDE SEQUENCE.
RA Waterston R.H.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.K.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC062022; AAX93124.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 16
SQ SEQUENCE 16 AA; 1801 MW; F5D5B8263B966EC8 CRC64;

Query Match 19.8%; Score 18; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 7.4e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 EDPGKQL 11
Db 4 KQGAQM 10

RESULT 15
O7M2K8 RABIT
ID O7M2K8_RABIT PRELIMINARY; PRT; 16 AA.
AC O7M2K8;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Alkaline phosphatase (EC 3.1.3.1).
OS Oryctolagus cuniculus (Rabbit)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=91112827; PubMed=1989515;
RA Fujimori-Arai Y., Koyama I., Hirano K., Sakagishi Y., Komoda T.;
RT "Purification and partial characterization of intestinal-like alkaline
RT phosphatase in rabbit kidney."
RL Arch. Biochem. Biophys. 284:320-325(1991).
DR PIR; S13898; S13898.
DR GO; GO:0004035; F:alkaline phosphatase activity; IEA.
SQ SEQUENCE 16 AA; 1973 MW; E9E78040172D8E38 CRC64;

Query Match 19.8%; Score 18; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EDP 7
Db 7 EDP 9

Search completed: May 15, 2006, 16:38:59
Job time : 226 secs
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